Institut für molekulare Mechanismen bei Krankheiten
der Vetsuisse-Fakultät Universität Zürich

Direktor: Prof. Dr. med. vet. Dr. phil. II Michael O. Hottiger

Arbeit unter wissenschaftlicher Betreuung von
Dr. sc. nat. Deena Leslie Pedrioli

Identification of the whole blood protein ADP-ribosylome under sepsis conditions in pigs

Inaugural-Dissertation

zur Erlangung der Doktorwürde der
Vetsuisse-Fakultät Universität Zürich

vorgelegt von

med. vet. Stephanie Lüthi

Tierärztin
von Lauperswil, Bern und aus den Vereinigten Staaten von Amerika

genehmigt auf Antrag von

Prof. Dr. med. vet. Dr. phil. II Michael O. Hottiger, Referent
Prof. Dr. sc. nat. Urs Meyer, Korreferent

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Summary

While blood proteins are heavily investigated as biomarkers for different diseases, the modification state of such proteins is rarely analyzed. Here, we established a novel mass spectrometry-based workflow to identify in vivo ADP-ribosylated blood proteins of LPS-treated pigs as a model for human systemic inflammatory response syndrome. We found that ADP-ribosylated proteins are rapidly demodified after sample collection by phosphodiesterases and ADP-ribosylhydrolases in the plasma, and thus to prevent demodification, we immediately denatured blood samples after collection with guanidine hydrochloride. Moreover, we improved the enrichment protocol of modified peptides via ADP-ribosylome specific LC/MSMS by depleting free ADP-ribose from samples prior to enrichment. This led to the identification of 44 ADP-ribosylated proteins in LPS-treated and 38 in control pigs. These proteins were cross-referenced with the plasma proteome, to determine which of the modified proteins belong to the plasma fraction of the blood, leading to the identification 12 ADP-ribosylated plasma proteins in LPS-treated pigs and 13 in control group pigs. Overall, we developed a novel method for identifying ADP-ribosylated blood proteins and characterized the whole blood and plasma protein ADP-ribosylomes of LPS-treated and control pigs. Further characterizing the blood ADP-ribosylome can help unravel the molecular mechanisms that drive sepsis.

Keywords: ADP-ribosylation, sepsis, whole blood lysate, NAD

Zusammenfassung

Blutproteine werden oft als Biomarker für verschiedene Krankheiten analysiert, aber deren post-translationelle Modifikationen werden selten untersucht. Wir entwickelten ein neues, Massenspektrometrie-basiertes Protokoll um *in vivo* ADP-ribosylierte Blutproteine in LPS-behandelten Schweinen zu identifizieren, welche als Modell für humanes systemisches inflammatorisches response Syndrom dienen. Da ADP-ribosylierte Proteine nach der Blutprobenentnahme rasch durch Phosphodiesterasen und ADP-ribosylhydrolasen demodifiziert werden, denaturierten wir die Blutproben direkt nach der Entnahme mit Guanidinhydrochlorid. Ein optimiertes Anreicherungsprotokoll bei welchem freie ADP-ribose depletiert wird, wurde entwickelt um die Peptidanreicherung für die Detektion via ADP-ribosylom-spezifischer LC-MS/MS zu verbessern. Mit diesem Protokoll wurden 38 modifizierte Blutproteine in gesunden und 44 in LPS-behandelten Schweinen identifiziert. Durch Vergleichen dieser Blutproteine mit dem Plasmaproteom, definierten wir das plasmaspezifische ADP-ribosylom: 13 modifizierte Proteine wurden in gesunden und 12 in LPS-behandelten Schweinen identifiziert. Zusammengefasst entwickelten wir eine neue Methode um ADP-ribosylierte Blutproteine zu identifizieren und charakterisierten erstmals das Vollblut- und Plasma-ADP-ribosylom von gesunden und LPS-behandelten Schweinen. Weiterführende Untersuchungen dieser Proteine könnten helfen, die molekularen Mechanismen von Sepsis besser zu verstehen.

Stichwörter: ADP-ribosylierung, Sepsis, Vollblut, NAD

Identification of the whole blood protein ADP-ribosylome under sepsis conditions in pigs

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1. ABSTRACT

While the analysis of blood proteins as biomarkers for different diseases is common nowadays, the modification state of such proteins is only rarely addressed. We observed that ADP-ribosylated proteins are rapidly demodified after blood sample collection due to active phosphodiesterases and ADP-ribosylhydrolases in the plasma, thus, requiring an optimized collection procedure for this PTM to prevent demodification. Here, we established a novel mass spectrometry based workflow to identify blood proteins that are ADP-ribosylated in healthy and lipopolysaccharide treated pigs *in vivo*, that serves as a model for human systemic inflammatory response syndrome. To this extent, blood samples including all cells and soluble proteins were immediately denatured with guanidine hydrochloride after collection to prevent post-sampling demodification. Moreover, an improved enrichment protocol that depletes free ADP-ribose from samples was established to enhance ADP-ribosylated peptide enrichment and identification rates in the whole blood lysates via ADP-ribosylome specific LC/MS-MS. Application of this modified protocol led to the identification of a total of 38 ADP-ribosylated proteins in healthy pigs and 44 in LPS-treated pigs. By cross-referencing these proteins with the corresponding plasma proteome, we determined which of the ADP-ribosylated proteins belong to the plasma fraction of the blood. This led to the identification of 13 ADP-ribosylated plasma proteins in healthy pigs and 12 in LPS-treated pigs. In summary, we developed a novel method for identifying ADP-ribosylated blood proteins and characterized the whole blood and plasma protein ADP-ribosylomes of healthy and LPS-treated pigs. This study thus contributes to the rapidly developing field of ADP-ribosylation and further characterization of the newly identified blood ADP-ribosylome will potentially help unravel the molecular mechanisms that drive SIRS and sepsis, two of the major health threats today.

Keywords: ADP-ribosylation, systemic inflammatory response syndrome, sepsis, whole blood lysate, plasma, histidine

2. INTRODUCTION

The clinical condition of systemic inflammatory response syndrome (SIRS) or sepsis is caused by pathogen-associated molecular pattern (PAMP) molecules, including lipopolysaccharide (LPS) [1]. These molecules interact with toll-like receptors (TLRs) on host immune cells, which triggers increased production of pro-inflammatory cytokines by immune cells circulating in the blood [2, 3]. Studies suggest that during sepsis, control of the primarily physiological host response to the infection is lost, which causes a multitude of systemic dysfunctions that ultimately lead to multi-organ failure and the resulting high mortality rates [4]. Although sepsis has been extensively studied, the specific molecular mechanisms that drive multi-organ failure and eventual death are not fully understood [4, 5]. As sepsis is one of the leading causes of death in humans, developing a reproducible study system and accurate diagnostic tools that allow sepsis detection at early stages is critical to facilitate appropriate therapeutic interventions and further therapeutic developments [5]. Porcine pleuropneumonia, a highly infectious disease in pigs that is caused by *Actinobacillus pleuropneumoniae*, could serve as a model for human SIRS and sepsis [6]. LPS derived from *A. pleuropneumoniae* has been shown to induce inflammatory responses by triggering alveolar macrophages to overproduce proinflammatory cytokines like IL-1B, IL-6 and TNFα [7]. This proinflammatory cytokine influx, combined with the occurrence of typical clinical symptoms such as fever, and elevated heart rate and respiratory rates match the defined criteria of human SIRS [3, 6]. Studies highlighting the similarity between the proteome of the domestic pig (*Sus scrofa domesticus*) and humans further emphasize the potential of pigs as model systems for human patients, especially for infectious disease and inflammation research [8].

Plasma is a readily accessible matrix for protein and biomarker research, and the plasma proteome has been extensively studied in humans, and various animals including pigs, under both healthy conditions and during the acute phase reaction; which is a complex early defense

mechanism that the body mounts in response to a triggering event like infection or inflammation [9, 10]. Plasma proteins whose abundances increase in response to inflammation or tissue damage have been termed positive acute phase proteins (pAPPs). Modern medicine relies on the detection of these few pAPPs to distinguish between healthy and diseased human patients on an individual basis, as well as large scale monitoring of herd health in farm animals [10]. However, the abundance of plasma proteins is not the only relevant feature; their modification states have also been previously studied as protein function can be regulated by PTMs [11]. These studies have led to the discovery of glycosylated proteins as prognostic markers for certain cancer types and phosphorylated proteins as prognostic markers for different diseases [12, 13]. The role of other PTMs in plasma have not yet been examined.

ADP-ribosylation is a dynamic and reversible PTM that transfers one (MARylation) or multiple (PARylation) ADP-ribose moieties from NAD^+ to an amino acid acceptor site of a target protein [14]. The possible acceptor amino acids include lysine, arginine, aspartic acid, glutamic acid, cysteine, and serine, as well as the recently discovered tyrosine and histidine [15-20]. Different ADP-ribosyltransferases (ARTs) have been described to MARylate or PARylate proteins. These enzymes are grouped into three subgroups based on their structural similarities to either diphtheria-toxin (ARTDs), cholera-toxin (ARTCs) or sirtuins [21]. Other enzymes are able to either hydrolyze the PAR chains (i.e. PARG), leaving a single ADP-ribose moiety bound to the protein, or are able to erase MARylation from proteins [22]. ADP-ribosylation plays a crucial role in many cellular processes including regulation of the inflammatory response within cells [23]. In contrast to the well-described role of ADP-ribosylation in such cellular mechanisms, its role in blood remains mostly uncharacterized. So far there has only been a single study reporting a correlation between non-enzymatic ADP-ribosylated serum proteins and cancer, but studies have not yet linked blood and/or plasma protein ADP-ribosylation to inflammatory diseases such as sepsis [24].

Here, we observed that serum prepared via standard methods identified very few ADP-ribosylated proteins by LC-MS/MS. This led us to first establish various *ex vivo* biochemical assays to determine whether ADP-ribosyltransferases and -hydrolases were present and active in the serum/plasma. We found that ADP-ribosylation could be induced by adding NAD^+ to heat-denatured plasma samples, however it remained unclear whether the observed increase was non-enzymatic or ADP-ribosyltransferase mediated. Furthermore, we found that erasers were active in the blood. Together, these assays demonstrated that proteins are rapidly demodified after blood sample collection prior to MS sample preparation and that standard blood sample collection techniques should be modified in order to maintain the modification state of proteins at the exact timepoint of blood sample collection. To this extent we collected blood samples from healthy and SIRS and sepsis model LPS treated pig both before and after NaCl or LPS injections and immediately denatured half of the blood sample with guanidine hydrochloride (GndHCl) to avoid demodification. The other half of the blood sample was used to prepare plasma. Before analyzing these samples via mass spectrometry (LC-MS/MS), we additionally improved the peptide enrichment workflow by reducing PAR chains to MAR before trypsin digestion and depleted free ADP-ribose to enhance ADPr-modified peptide enrichment efficiencies. We then applied the optimized workflow to the denatured porcine blood samples to determine which proteins were ADP-ribosylated *in vivo* and how modification states differed between healthy and LPS-treated pigs. Finally, we compared the whole blood ADP-ribosylome to the corresponding plasma proteome to tease out which of the modified proteins belong to the cellular fraction of the blood and which to the plasma fraction. Interestingly, in addition to serine and lysine, histidine was identified as a common ADPr-acceptor amino acid in both control and LPS-treated pigs samples, suggesting that the main writer of ADP-ribosylation in the blood has yet to be identified.

3. MATERIALS AND METHODS

LPS-induced SIRS study system

This study was conducted in accordance with the Swiss animal protection ordinance, under animal experimentation license number ZH046/17. 4-6 week old pigs (n=10) were housed at the University of Zurich animal hospital and randomly allocated to either the control (n=5) or LPS group (n=5). The LPS trial lasted for a total of 10 days. From day 1 to 8 pigs were allowed to adapt to the new housing facilities and their clinical conditions assessed daily based on dyspnea, coughing, lung auscultation, nasal discharge and behavior parameters, which allowed us to define their health status and determine if individual animals should be removed from the trial. None of the pigs entered into the study showed signs of porcine pleuropneumonia, thus no animals were removed from the trial. On day 9 all pigs were again examined clinically, weighed, and a first blood sample collected. Pigs were then injected intramuscularly with 0.9% NaCl-solution (control group, 250 μl) or with LPS derived from *A. pleuropneumoniae* (treatment group, 250 μl 25% Montanide containing 31.3 μg LPS). Following the injections, core body temperatures were assessed after 4, 6, 8, and 10hrs and a second blood sample was collected from each pig at the 8hr timepoint.

Blood sample collection and sample preparation

6 mL of venous blood were collected from each pig at both timepoints as previously described [25]. After collection, samples were immediately split into 3 fractions: 2 mL were transferred to heparin and EDTA tubes respectively (both BD, USA). Heparin samples were then centrifuged (1000x g, 10 min), the plasma separated from the cell pellet and stored at -80 °C for downstream plasma proteome analyses. The EDTA samples were kept at RT and immediately processed for hematological analyses. The remaining 2 mL were added to falcon tubes containing 4 mL of 6M GndHCl and mixed thoroughly to denature the samples. These

whole blood lysates (WBL) were then heated to 95 °C for 10 min and stored at -80 °C until LC-MS/MS ADP-ribosylome analysis.

Western blot analysis

For Western blot (WB) analyses, samples were prepared using standard SDS-PAGE and blotting techniques. Membranes were incubated with blocking solution (3% BSA in TBS-T (0.15 M NaCl, 10 mM Tris pH 7.5, 0.05% Tween-20)) for 1-2hrs at room temperature (RT), and subsequently incubated overnight at 4 °C with the primary anti-ADPr-antibody (diluted 1:10'000 in TBS-T; Cell Signaling Technology, USA). Membranes were washed 3x for 5 min with TBS-T and incubated IRDye goat-anti-rabbit IgG secondary antibody (diluted 1:15'000 in TBS-T, LI-COR Biosciences, USA) for 1hr at RT and washed again as described before scanning (Odyssey Scanner, LI-COR Biosciences, USA).

Auto-modification of ARTD1

ARTD1 (formerly PARP1, Trevigen, USA) was auto-modified by incubating 10 U ARTD1 with or without 4.5 μg HPF1, 2 μg activated DNA and 5 μM NAD^+ in 1x Trevigen PARP1 reaction buffer at 25 °C for 20 min. The reaction was stopped by adding SDS-LB (final concentration 1x) and heating to 95 °C for 10 min. Alternatively, for the experiment characterizing eraser activity in plasma, ARTD1 (in-house) was auto-modified by incubating 0.875 μg ARTD1 with or without 100 μM NAD^+, activated DNA (1 μg/reaction) in 1x RB (50 mM Tris-HCl pH 7.4, 4 mM $MgCl_2$, 250 μM DTT) at 37 °C for 1 hour (total volume of 25 μL per reaction).

Induction of ADP-ribosylation *ex vivo* via heat denaturing

25 μl of porcine plasma were heat denatured (95 °C, 10 min) in presence or without 100 μM NAD^+ and subsequently incubated at 37 °C overnight to induce ADP-ribosylation. Samples were then diluted with 50 mM Tris pH 7.4 and 6x SDS-LB was added (final concentration 1x), sonicated and heated (95 °C, 10 min) before storing at -20 °C. Samples where GndHCl was added were subjected to a buffer exchange regime using Microcon-10 kDa centrifugal filter units. Centrifugation (14'000x g, 20 min, RT) and washing 2 times with 100 μL 50 mM Tris pH 7.4 led to buffer exchange and SDS-PAGE compatibility. The resulting samples were resuspended in 25 μL Tris pH 7.4 and prepared as described above.

Induction of ADP-ribosylation *ex vivo* via hARTC1

DC27.10 cells expressing human ARTC1 (hARTC1) on the cell membrane (kindly provided by F. Koch-Nolte) were grown in RPMI medium (1x) with GlutaMax supplement (Thermo Fisher Scientific Inc., USA) and with 5% fetal calf serum at 37 °C. 2 x 10^6 cells were collected via centrifugation (300x g, 5 min, 4 °C) and gently resuspended in 100 μl of plasma. 100 μM NAD^+ was then added to the cell suspension and samples were incubated at 37 °C for 1hr. The resulting plasma was then collected by centrifugation (300x g, 5 min, 4 °C) and analyzed via WB.

Cell culture and ADPr-peptide enrichment

HeLa cells were cultured and treated with H_2O_2 as previously described and the lysates were used to test the new workflow and served as positive and negative controls for LC-MS/MS of the WBLs [16]. Wildtype and an evolved Af152 macrodomain, with 1000-fold enhanced binding affinity to ADP-ribose (*Nowak et al.*, manuscript under revision), were expressed and purified as previously described [26]. Binding and crosslinking of the GST-Af1521 fusion

proteins to Glutathione Sepharose 4B beads, peptide enrichment ("standard workflow") and pre-MS clean-up using stage tips were performed as described in [26-28]. After elution, samples were resuspended to 12 μL in MS-buffer (3% ACN, 0.1% formic acid), vortexed briefly, sonicated (10 min, 100%, 25 °C), and centrifuged (16'000x g, 2 min, RT) before MS analysis.

For the new workflow established in this study, samples were diluted to 0.2M GndHCl using 1x PARG buffer (50 mM Tris-HCl pH 8.0, 50 mM NaCl, 10 mM $MgCl_2$, 0.25 mM DTT), and 4.2 μg PARG (in-house) per 10 mg protein and 10 μL of Benzonase (Merck Millipore, GER) per 30 mL were then added to each sample. The samples were incubated at 37 °C for 1hr. Samples were then trypsin digested as per the standard protocol and all subsequent steps performed as previously described. WBL samples collected during the LPS trial were prepared using the new workflow with additional high pH (HpH) and low pH (LpH) fractionation on MicroSpin C18 columns (Nest Group Inc., USA) as described in [20]. Samples were eluted from the HpH column using three different percentages of ACN (7%, 15%, and 50% in 20 mM NH_4OH) and from the LpH column using one condition containing 60% ACN / 0.1% TFA.

Preparation of plasma input samples for MS analyses

Plasma input samples were prepared via filter aided sample preparation (FASP) [29]. Briefly, samples were denatured using GndHCl lysis buffer (6 M GndHCl, 5 mM TCEP, 10 mM CAA, 100 mM Tris-HCl pH 8.0, final concentration 4M), heated (10 min at 99 °C) and sonicated. 100 μg of protein were transferred onto the Microcon-10 kDa centrifugal filter unit, centrifuged (14'000x g, 20 min, RT) and washed 3 times with 100 μL 0.5 M NaCl (centrifugation as described). 120 μL of 50 mM ammonium bicarbonate were added to the filter unit and centrifuged as described above. Trypsin (Promega, USA) was added at a 1:25 ratio (μg trypsin: μg protein), the filter units sealed and incubated overnight (37 °C, 16-20 hrs, 300 rpm). The filter units were then centrifuged as described and the columns re-eluted using 80 μL 50 mM

ammonium bicarbonate solution. The eluate was acidified with 10% TFA to a pH of 3-4 and the samples were then further prepared for MS analysis via Zip Tip clean-up according to the Millipore zip tip user guide (Merck Millipore, GER). Samples were resuspended in MS-buffer and processed as described for ADPr samples.

Mass spectrometry and data analysis

LC-MS/MS analyses of ADP-ribosylated peptides were performed using the ProductPreview method as described in Bilan *et al*. at the Functional Genomics Center Zurich using the Orbitrap Fusion Lumos mass spectrometer (Thermo Fisher Scientific Inc., USA) [30]. Briefly, 2-5 μL of the prepared peptides solutions were eluted over 112 min at 300 nL/min, with ACN concentrations ranging from 5% to 95%. Initial high energy HCD scans were then applied to detect unique fragmentation ions of ADP-ribose, which in turn triggered product-dependent MS-events. Parallel high resolution HCD and EThcD scans were acquired to maximize peptide sequence coverage and PTM localization confidences [30].

Downstream data analysis was performed as previously described [30]. The HCD and EThcD deconvoluted separated .msg files were searched against the UniProt database for human and porcine proteins respectively using Mascot, and the following search parameters were applied: trypsin digests with up to 5 missed cleavages, carbamidomethyl as a fixed modification on cysteine (C), acetyl (protein N-term), oxidation (M), and ADPr_HCD_249_347_583 DEHKRSY (HCD scans, neutral losses defined in [31] and *Gehrig et al*., manuscript under revision) or ADP-Ribosyl EThcD (for EThcD scans) as variable modifications, peptide tolerance = 10 ppm, number of ^{13}C = 1, peptide charge = $2^+/3^+/4^+$, MS/MS tolerance = 0.05 Da [32]. Briefly, the resulting files were filtered to include only peptides with one or more ADP-ribose modifications, peptide scores > 15 (WBL samples) or > 20 (HeLa cell lysates) and peptide expect values < 0.05. For ADP-ribose acceptor site

localizations, the list of modified peptides was further filtered based on peptide variable modification confidence values > 95%. MS analyses of input proteome samples were performed using standard data dependent acquisition (DDA) methods. The following search parameters were used to search input proteome deconvoluted data: trypsin digests with up to 5 missed cleavages, carbamidomethyl as a fixed modification on cysteine (C), acetyl (protein N-term), oxidation (M), peptide tolerance = 10 ppm, number of $^{13}C = 1$, peptide charge = $2^+/3^+/4^+$, MS/MS tolerance = 0.5 Da [32]. Plasma proteome search results were filtered as described above for peptide score and peptides expect values, without regard to ADP-ribosylation.

Statistical analysis

Statistical analyses were performed using R version 3.5.2 [33]. Differing core body temperatures and total leukocyte amounts of control/LPS-treated pigs were tested for their statistical significance at each time point (0hr, 4hrs, 6hrs, 8hrs and 10hrs post injection or before and after injection, respectively). Normal distribution was first tested using a ShapiroWilk normality test and subsequently a two-tailed, unpaired t-test (normal distribution) or a MannWhitney U test (non-normal distribution) was applied. Differences in peptide presence were analyzed by creating 2 x 2 contingency tables for each ADP-ribosylated peptide found in plasma samples and then categorizing the data as either (1) control conditions or LPS treatment and (2) number of pigs where the peptide was detected or not detected. Due to a non-normal distribution as well as unequal and small sample sizes a Fisher's exact test was used for further analysis. All results were considered significant for p-values < 0.05.

4. RESULTS

LPS treatment significantly increases core body temperature and total leukocyte numbers in pigs

The LPS-induced SIRS study system consisted of an LPS trial during which 10 pigs were injected with either NaCl (n=5) or LPS (n=5) solutions and blood samples were collected at different timepoints (Table 1). To determine how pigs reacted to a single LPS injection (31.3 μg) the core body temperature and total number of leukocyte were analyzed before and after injection, as these are two key symptoms of SIRS. LPS-treated pigs displayed significant ($p < 0.05$) increases in core body temperature 4, 6, 8, and 10hrs after injection compared to the control group (Suppl. Figure 1A). The total amount of white blood cells also increased significantly in the LPS treatment group after injection, while in the control group no significant changes were observed before or after NaCl injection (Suppl. Figure 1B). Additionally, protein concentrations were assessed for each pig before and after the LPS or NaCl injections. No significant differences were observed between the two groups at either timepoint (Suppl. Figure 1C). Together, these data indicate that the established porcine LPS-induced SIRS model elicits clinical and hematological reactions similar to human SIRS.

Optimization of the MS-based workflow to allow detection of low abundant ADP-ribosylated proteins

Preliminary experiments with serum samples from NaCl- and LPS-treated pigs revealed that the levels of ADP-ribosylation were very low, even below the level of untreated HeLa cell culture samples (data not shown). We, therefore, first optimized the standard ADP-ribosylome workflow to increase enrichment efficiency prior to MS-based analysis of ADP-ribosylation; this was done using H_2O_2 treated HeLa cells [26]. Here, we included one major change to the established standard workflow. We brought the PARG/Benzonase treatments of the lysates

forward to the first step of the sample preparation protocol in the hope that this would improve trypsin digest efficiency and modified peptide enrichment (Suppl. Figure 2). This was rationalized based on studies that have recently demonstrated that S-ADPr modifications are typically found within KS and RS motifs, thus reducing PAR chains to MAR modifications prior to trypsin digestion could improve protein-to-peptide digestion [18]. In addition, we also reasoned that C18 column clean-up after PARG digest would eliminate most of the free ADP-ribose prior to ADPr-peptide enrichment. This could provide an additional advantage, as competitive binding between the free ADP-ribose and ADPr-peptides to the Af1521 macrodomains would be reduced and, thus, MARylated peptide enrichment efficiencies should increase.

To determine if the protocol modification improved ADP-ribosylome coverage, we compared the unique peptides, unique modification sites (> 95% localization confidence) and unique modified proteins identified for the standard workflow and new workflow (Figure 1A). The new workflow outperformed the standard workflow considerably by identifying ~3x more modified peptides, ~2x more unique modification sites and ~2.5x more proteins, suggesting that this modification provided an experimental advantage (Figure 1A). Indeed, application of the new workflow led to the identification 88 modified proteins, while the standard workflow only identified 34 ADP-ribosylated proteins (Figure 1B). Comparison of the standard workflow and new workflow coverages revealed that only 5 proteins (5.4%) were uniquely identified in samples using the standard workflow, indicating that the sample preparation changes made for the new workflow do not bias peptide enrichment or modified protein identifications. Importantly, the new workflow identified 59 proteins (63.4%) that were not detected with the standard workflow and greatly reduced the number of mis-cleaved peptides (Figure 1C), demonstrating that our workflow modifications increased ADP-ribosylome coverage considerably (Table 2).

In an attempt to further increase our ADP-ribosylome coverage, we applied additional sample preparation improvements that were recently established [20]. This included lowering acetonitrile concentrations during the SepPak clean-up step to ensure that only the highest quality peptides were eluted from the columns prior to ADPr-peptide enrichment. Second, we applied the HpH/LpH fractionation protocol to reduce sample complexity and improve peptide sequencing during MS analysis. These modifications were again assessed using HeLa H_2O_2 treated cell lysates and applied to the new workflow protocol that we developed above. Indeed, including these additional sample preparation modifications increased ADP-ribosylated peptide, modification site and protein detection rates by 68.7%, 52.9%, and 69% respectively (Suppl. Figure 3A & B), indicating that including these additional sample preparation modifications further increases ADP-ribosylome coverage. In light of these promising findings, the new workflow with fractionation was selected for MS sample preparation for the LPS trial blood samples.

ADP-ribosyltransferases are present and active in porcine plasma samples

Unfortunately, very few ADP-ribosylated proteins were identified when this optimized ADP-ribosylome MS-workflow was applied to serum samples collected from a preliminary LPS trial (data not shown). Therefore, we established various biochemical assays to determine if the ADP-ribosylation states of plasma/serum proteins could be altered during sample collection and preparation. First, to demonstrate that the anti-pan-ADPr-antibody detects both PARylation and MARylation modifications, Western blot (WB) analyses were carried out on ARTD1 (also known as PARP1) samples that were modified *in vitro* via incubation with NAD^+, activated DNA and/or HPF1 [34]. Auto-modification and strong PARylation of ARTD1 was detected when the enzyme was incubated with NAD^+ and activated DNA, and, as previously demonstrated, the presence of HPF1 strongly shifted the modification state of ARTD1 from

PARylation towards MARylation and shorter PAR chains (Figure 2A, Suppl. Figure 5A) [19]. Little or no ADP-ribosylation was detectable via WB when ARTD1 was incubated without NAD^+. Together, these data confirm that this antibody can be used in WBs to detect all forms of ADP-ribosylation.

Next, we determined whether ADP-ribosyltransferases are present in plasma samples and if they were active under ADP-ribosylome MS sample preparation conditions. Plasma samples from healthy pigs were heat-denatured or denatured with 6M and 0.2M GndHCl, and then incubated overnight at 37 ºC in the presence or absence of NAD^+. WB analysis of the resulting samples revealed that heat-denaturing at 95 ºC for 10 min, combined with subsequent overnight incubation at 37 ºC with NAD^+, resulted in extensive ADP-ribosylation that was not induced in the absence of exogenous NAD^+ (Figure 2B, Suppl. Figure 5B). These findings suggest that either ADP-ribosylhydrolases present in plasma are more susceptible to heat-denaturing or that heat-denaturing inactivates both plasma ADPr-writers and -erasers, but creates an environment ideal for non-enzymatic ADP-ribosylation modification. Addition of GndHCl to the sample at a final concentration of 0.2M reduced the observed increase in ADP-ribosylation by about half, while full denaturing condition (6M GndHCl) inhibited ADP-ribosylation completely. These results suggest that adding GndHCl to blood or plasma samples at a final concentration of 6M could preserve the ADP-ribosylation state of the sample.

Endogenous erasers of ADP-ribosylation are active in blood samples and rapidly reduce ADP-ribosylation after sample collection

In light of the findings presented above, we wanted to determine whether plasma protein ADP-ribosylation could be rapidly erased after sample collection and/or during plasma preparation. ADP-ribosylation was induced *ex vivo* in healthy pig plasma samples via incubation with NAD^+ and DC27.10 cells that ectopically express the R-ADPr-specific ADP-ribosyltransferase

hARTC1 [35]. After modification, the cells were removed by centrifugation and the plasma incubated at 37 ºC for 15 min, 1hr, 4hrs and overnight (16hrs) to assess if the induced ADP-ribosylation could subsequently be erased. Indeed, a strong decrease of plasma protein ADP-ribosylation was observed already after 1hr and 4hrs. Most strikingly, ADP-ribosylation levels were reduced to those of untreated samples when the DC27.10 cell modified plasma samples were incubated overnight at 37 ºC (Figure 2C (left panel), Suppl. Figure 5C (left panel)), suggesting that R-ADPr modifications are rapidly erased in plasma and blood samples.

Nevertheless, it remains unclear if the observed demodification was mediated by classic ADP-ribosylhydrolases present in the plasma. Indeed, studies have demonstrated that phosphodiesterases (PDEs), enzymes are known to reduce ADP-ribose to phosphoribose, are abundant in the blood and, thus, could also be responsible for the observed loss of plasma protein ADP-ribosylation [36, 37]. Based on this hypothesis, we repeated the experiment described above (Figure 2C (right panel), Suppl. Figure 5C (right panel)), but included cAMP in the reactions as this metabolite can compete with ADP-ribose as a PDE substrate. Interestingly, addition of 100 μM cAMP partially blocked the observed demodification for the first hour of incubation (Figure 2C, right panel). Together, these findings indicate that PDEs present in the plasma actively erase mono-ADPr plasma protein modifications within 1hr at 37 ºC. These finding are critical, as blood collection and plasma preparation times fall within this time frame; thus, endogenous ADP-ribosylation modifications could be substantially reduced, or entirely lost, using standard sample preparation methodologies.

Having established that R-ADPr modifications could be demodified in the plasma, we determined if this also holds true for other ADPr-amino acid acceptor modifications. To address this, we used ARTD1, which is mainly modified on serine (S) residues [38]. ARTD1 was auto-modified in the presence of NAD^+, activated DNA and HPF1. Following auto-modification, PJ34 (to inhibit further modification) and plasma were added, and the samples incubated for

1hr, 4hrs, and overnight (16hrs) at 37 °C. These samples were then analyzed via WB to determine if the amount of ADP-ribosylation decreased in the presence of plasma (Figure 2D, Suppl. Figure 5D). Indeed, ARTD1 ADP-ribosylation states gradually decreased when plasma was present; this was most evident following overnight incubation at 37 ºC. Together, these findings suggest that plasma ADP-ribosylation demodification is not specific to one ADPr-amino acid acceptor linkage and it is likely that all ADPr-acceptor site modifications can be erased in the plasma. Moreover, these results demonstrate that ADP-ribosylhydrolases and PDEs are likely present in plasma samples and that *in vivo* ADP-ribosylated plasma proteins are demodified shortly after blood sampling prior to MS sample preparation. Therefore, optimization of the sample collection is crucial to preserve *in vivo* ADP-ribosylation.

MS analysis of the *in vivo* whole blood ADP-ribosylome identifies 38 modified proteins in healthy pigs and 44 in LPS-treated pigs

To identify the whole blood ADP-ribosylome of healthy and LPS-treated pigs via LC-MS/MS, we collected two different types of samples from the animals. First, whole blood lysates (WBLs) were generated by immediately denaturing the samples with 6M GndHCl after collection. These samples were processed for LC-MS/MS analysis using the new ADP-ribosylome enrichment workflow with fractionation presented above (Figure 1, Suppl. Figure 1). Second, to define the plasma-specific ADP-ribosylome, part of each blood sample was anti-coagulated and processed to plasma. The plasma proteomes of each of these samples were defined via standard shot gun LC-MS/MS methods.

We compared the amount of unique peptides, unique modification sites (> 95% localization confidence) and unique modified proteins identified in the WBLs of NaCl- and LPS-treated pigs and found that there were no significant differences in the amounts of either ADP-ribosylated peptides, unique modification sites or modified proteins between the two

groups (Figure 3A). A total of 64 ADP-ribosylated proteins were identified in the WBLs, 20 of which were uniquely found in the control group and 26 in the LPS-treated group respectively (Figure 3B). The modified proteins that were unique to the control group include proteins such as SENP5, HBE1, and RAD51D (Figure 3C, Table 3). While most of the proteins were only identified in 1 of the 5 control group pigs, the proteins MNS1 and YTHDC2 were found in 2 and 3 of these pigs respectively (Figure 3C). 26 of the 64 ADP-ribosylated proteins detected in WBLs were unique to the LPS-treated group, including proteins such as SATB2, CA1, and HES2 (Figure 3D, Table 4). Similar to the trend observed for proteins unique to the control group, most of these modified proteins were again identified only for 1 of the 5 LPS-treated pigs, whereas 2 proteins (ARRDC5 and MYO3B) were identified for 2 pigs each (Figure 3D). Interestingly, 18 modified proteins were identified in both NaCl- and LPS-treated pigs including the porcine acute phase protein AHSG as well as hemoglobin subunits alpha and beta (Figure 3E, Tables 3 and 4). However, due to small sample numbers (n=5), no statistical differences in regard of the ADP-ribosylated proteins were found when analyzing the whole blood lysates.

Comparison of the WBL ADP-ribosylome and input plasma proteome identifies 15 modified plasma proteins

To determine which of the modified proteins identified in the WBLs belong to the plasma fraction of the blood, we performed single-shot plasma proteome analyses and identified 828 plasma proteins in healthy and 636 in LPS-treated pigs respectively (Figure 4A, Table 5). These two plasma proteomes were combined to generate a pig plasma reference proteome that contained 1055 unique proteins. This reference plasma proteome was then compared to the whole blood ADP-ribosylomes, which allowed us to identify the *in vivo* plasma ADP-ribosylome (Figure 4B). Overall, the control and LPS-treated groups showed very similar

amounts of unique peptides, unique modification sites (> 95% localization confidence), and ADP-ribosylated protein identifications, similar to the findings for the WBL ADP-ribosylome (Figure 4C). However, of the 13 ADP-ribosylated plasma proteins that were identified in healthy pigs and 12 in LPS-treated pigs, 3 were unique to the control group and 2 to the LPS-treated group (Figure 4D). The 3 proteins belonging to the control group only including biliverdin reductase B (BLVRB), Cache domain containing 1 protein (CACHD1) and hemoglobin subunit epsilon (HBE1) (Figure 3C) and the 2 modified plasma proteins unique to the LPS treatment group were carbonic anhydrase 1 (CA1) and an uncharacterized protein (Figure 3D). Due to small sample numbers (n=5), and the fact that some of these proteins were only identified in a single animal, differences in the presence of the 15 ADP-ribosylated plasma proteins were not significant.

In addition, functional protein association network analyses (STRING) were performed for the ADP-ribosylated proteins identified in the WBL samples as well as the plasma and cellular fractions individually. Functional enrichments found in the WBL network included oxygen transport (HBA, HBB, and HBE1) as well as nicotinamide nucleotide metabolic process (MDH1 and GAPDH) (Figure 5) [39]. When analyzing only the cellular fraction of the blood ADP-ribosylome, we identified functional enrichment for microtubule associated proteins (BICD1 and BICD2) [39]. Within the plasma ADP-ribosylome, multiple molecular processes such as oxygen transport (HBB and HBE1), organonitrogen compound metabolic process (ALDH9A1, MDH1, GAPDH, and CACHD1), oxidation reduction process (ALDH9A1, MDH1, and GAPDH) as well as nicotinamide nucleotide metabolic processes (MDH1 and GAPDH) were functionally enriched [39]. In conclusion, applying the new workflow with fractionation to the WBL samples helped us identify the first ever blood ADP-ribosylome and the results indicate that there are most likely biologically relevant differences in the WBL and plasma ADP-ribosylomes of mock treated and LPS-treated pigs.

Serine and histidine are the most abundant ADP-ribose acceptor sites in WBL and plasma

When analyzing protein ADP-ribosylation, the acceptor amino acids are of great interest since their distributions can help define the ADP-ribosyltransferases that could write the observed modifications. Thus, we determined the number of unique modification sites with > 95% PTM localization confidence in the WBL samples (including cellular and plasma proteins) as well as the plasma ADP-ribosylome (plasma proteins only). Interestingly, H- and S-ADPr modifications were both equally abundant in control and LPS-treated pigs (Suppl. Figure 4A). While the search algorithm also identified Y-ADPr, R-ADPr, D-ADPr and E-ADPr, these sites were ~3-time more abundant in both control and LPS-treated WBL samples. Very similar distributions and amounts of unique acceptor sites with high PTM localization confidences were identified when analyzing the ADPr-acceptor sites of the plasma protein ADP-ribosylome (Figure Suppl. 4B). Together, these data demonstrate that the most prominent unique ADPr-acceptor sites with highest PTM localization confidence are indeed found within the plasma ADP-ribosylome and not the cellular fraction of the whole blood ADP-ribosylome. This could be due to the fact that plasma proteins, like HBB and AHSG are highly abundant and modified at multiple sites. Most interestingly, given that these results indicate that H-ADPr modifications are as abundant as S-ADPr modification, these data also suggest that the most active ADP-ribosyltransferase in the plasma has not yet been characterized.

5. DISCUSSION

In this study, we aimed to identify the whole blood and plasma protein ADP-ribosylomes in a porcine model for human SIRS and sepsis. To this extent, we first established the SIRS model by injecting pigs with either NaCl (control group) or *A. pleuropneumoniae*-derived LPS (treatment group) and monitored their clinical and hematological responses for 10hrs post-injection. Preliminary experiments identified very few ADP-ribosylated proteins in serum samples from LPS treated pigs, we thus optimized the current ADP-ribosylated peptide enrichment workflow for downstream LC-MS/MS analysis. This was achieved by reducing long PAR chains to MAR before tryptic digestion, which was subsequently followed by depletion of PARG-generated free ADP-ribose from the samples prior to ADPr-peptide enrichments. We assessed efficacy of these optimizations using HeLa H_2O_2 treated cell lysates, which is the gold-standard sample for ADP-ribosylome analyses within the field, and found that ADP-ribosylated protein identifications increased ~2.5x when compared to the current state-of-the-art ADP-ribosylome MS-workflow (standard workflow) [18, 20]. Unfortunately, applying this optimized workflow to serum samples from LPS-treated and healthy pigs failed to improve ADP-ribosylated protein identifications. This led us to establish various *ex vivo* biochemical assays to determine whether ADP-ribosyltransferases and -hydrolases were present and active in the plasma/serum. Interestingly, we found that ADP-ribosylation could be induced by adding NAD^+ to heat-denatured plasma samples and that *ex vivo* and *in vitro* induced ADP-ribosylation was efficiently erased after incubation periods between 1hr and 16hrs at 37 °C. These assays suggested that proteins are rapidly demodified after blood sample collection prior to MS sample preparation and that the sample collection protocol required optimization to maintain modification states at the time of sample collection. To this extent, we denatured blood samples from control and LPS-treated pigs immediately following collection and then defined the ADP-ribosylome of these whole blood lysates using the new ADPr-MS-

based workflow described above. This led to the identification of 38 ADP-ribosylated blood proteins in healthy pigs and 44 in LPS-treated pigs. To determine which of these ADP-ribosylated proteins were modified plasma proteins, we cross-referenced the whole blood ADP-ribosylomes with the total plasma proteome and identified 15 ADP-ribosylated plasma proteins, 10 of which were found in both groups, 3 that were unique to the control group and 2 to the LPS-treated group.

To improve the enrichment efficiency of the existing MS sample preparation workflow, we performed a PARG treatment prior to trypsin digestion and sample clean-up prior to ADPr peptide enrichment. We reasoned that i) reducing the long and/or branched PAR chains to MAR modifications before trypsin digestion would improve the accessibility of digestion sites within the proteins and that ii) eliminating the free ADP-ribose could provide an additional advantage, as competitive binding between the free ADP-ribose and the modified peptides to the Af1521 macrodomains would be reduced. Indeed, recent studies demonstrate that S-ADPr modifications are typically found within KS and RS motifs and, thus, reducing the large PAR chains could facilitate tryptic digestion, since trypsin is known to cleave peptide bonds after K and R [18, 40]. Introducing fractionation off of the C18 columns using different concentrations of ACN in either NH_4OH (HpH) or TFA (LpH) to the sample preparation workflow further improved ADP-ribosylome coverage most likely by reducing sample complexity as described for HeLa cells [41].

After identifying very few ADP-ribosylated proteins in preliminary experiments using the optimized new workflow enrichment protocol, we performed various *ex vivo* modification and demodification assays that, taken together, suggest that ADP-ribosyltransferases and erasers of ADP-ribosylation (including PDEs) are present and active in the blood, even after sample collection. To further assess the presence of these enzymes in the blood samples, we analyzed the reference plasma proteome with respect to known writers and eraser of ADP-

ribosylation and found that ARTC3 was present in all control and LPS pigs. ARTC3 has been previously identified in porcine muscle samples as well human plasma samples and is known to ADP-ribosylate arginine residues [42, 43]. However, only few arginine modifications were detected in the blood samples via MS analyses of, suggesting that either this enzyme is most likely not the main writer of ADP-ribosylation in the blood or that it is not entirely arginine specific, but can also modify other acceptor sites. Interestingly, one of the most abundantly modified amino acids in the ADP-ribosylomes of control and LPS-treated pigs was histidine, which is the most recently identified ADPr-acceptor amino acid [20]. This novel finding suggests that an uncharacterized ADP-ribosyltransferase could be present in the blood and responsible for the modification of histidine residues on these target proteins. Despite the fact that sirtuins and phosphodiesterases have been previously identified in human plasma, we did not identify any of the known ADP-ribosylhydrolases, or phosphodiesterases in the pig plasma samples analyzed here [42]. Since many known writers and erasers of ADP-ribosylation are localized within cells, they could be released into the blood after cell necrosis/lysis, and the resulting concentrations of writers and erasers in the plasma would most likely be very low, emphasizing the need for a highly sensitive method to detect these enzymes. Therefore, in depth analysis either via depletion and fractionation of the plasma proteome or parallel reaction monitoring (PRM)-MS could be applied to identify other writers or erasers that are present [44].

In order to fully characterize and understand the functionality and potential downstream effects of blood protein ADP-ribosylation, the identification of ADP-ribosylated proteins is key and needs to be established. The novel method described and tested in this study provides a first step towards analyzing *in vivo* ADP-ribosylated blood and plasma proteins at the timepoint of sample collection and avoids post-sampling demodification. The modified proteins identified provide a first description of the *in vivo* whole blood and plasma ADP-ribosylomes and could influence protein functions in various ways. For example, two of the most heavily modified

proteins found in WBLs of both control and LPS samples were hemoglobin subunits alpha and beta, which are known to interact with drugs along with their important role in oxygen transport [45]. Thus, ADP-ribosylation of the hemoglobin subunits could alter its binding affinity to drugs or oxygen, carbon dioxide and/or carbon monoxide similarly as described for different hemoglobin mutations resulting in low affinity O_2 binding due to its large size and structural interference [46]. Indeed, the peptides containing the histidine residues important for O_2 binding (His87 in HBA and His93 in HBB) were found to be modified in both control and LPS-treated pigs [47]. Furthermore, ADP-ribosylation could negatively affect the drug binding capabilities of hemoglobin, ultimately resulting in increased renal excretion of drugs, similar to what has been described for glycosylation of drug binding plasma proteins [48]. Other plasma proteins that were found to be ADP-ribosylated included AHSG, which was modified in all 5 control pigs, but only 2 LPS pigs. This protein is a secreted acute phase protein in pigs, and total concentration of AHSG is routinely measured in a clinical setting to roughly quantify ongoing inflammatory reactions [32, 49]. Examining the modification state of AHSG at different timepoints during infection as opposed to only measuring abundance in blood samples could potentially help determine duration and severity of bacterial infections in pigs and possibly even predict clinical deterioration early-on. To further investigate this hypothesis, a time-course study with a targeted approach for AHSG ADP-ribosylation could be applied to the LPS model system.

A possible mechanism leading to changes in ADP-ribosylation during severe SIRS or sepsis includes damage and intravascular decay of white blood cells, as well as the release of NAD^+ and intracellular ADP-ribosylation writers and erasers to the blood as a result of tissue damage and cellular necrosis. Since intracellular proteins such as histones have been shown to be released into the blood stream under SIRS-like conditions, it is entirely possible that the ADP-ribosyltransferases and -hydrolases are also released into the blood stream and are could

be responsible for the modification of blood proteins found only in LPS-treated pigs [50]. Accordingly, some of the proteins found in the plasma ADP-ribosylome are known intracellular proteins such as GAPDH, BLVRB, and MDH1, that were likely released into the blood stream after cell damage and could, thus, serve as a marker for cell lysis and severity of SIRS.

Even though no significant differences were detected between the control and LPS group due to small sample sizes, directly analyzing and validating the proteins that were found to be uniquely modified in healthy or LPS-treated pigs could serve as potential diagnostic markers in a clinical setting. First, the detection of these low abundant proteins could be increased by depleting high abundant blood proteins such as albumin in order to reduce the range of protein abundance and sample complexity [51]. The ADP-ribosylated proteins detected in plasma samples from LPS-treated but not healthy pigs could subsequently be validated as early biomarkers for SIRS. However, time- and cost-intensive LC-MS/MS is not feasible for routine clinical diagnostics. Rather, an easily applicable, time- and cost-efficient test such as an ELISA could be designed for a such validated targets. Many of the biomarkers currently validated for sepsis are not able to distinguish between infected and non-infected SIRS patients, and as a result, these diagnostic tests are not able to predict clinical deterioration [52]. Our novel method could be used to analyze plasma ADP-ribosylation patterns at multiple timepoints throughout sepsis development to determine if certain modified target proteins predict impending sepsis. Ideally, blood samples would be collected using the optimized sampling method at various timepoints before clinical diagnosis of sepsis and the ADP-ribosylome could be compared between patients that develop sepsis and those who do not. Furthermore, the survival rate relative to ADP-ribosylation abundance could be analyzed and potentially applied to determine prognosis on an individual patient basis.

In conclusion, this study contributes to the rapidly developing field of ADP-ribosylation. To the best of our knowledge, no whole blood or plasma ADP-ribosylomes have

been identified and published so far. The workflow developed in this study combined with the improved blood sampling technique has led to the identification of the first whole blood and plasma ADP-ribosylome using *Sus scrofa domesticus* as a model organism for human SIRS. Moreover, the novel method developed to identify the exact *in vivo* state of ADP-ribosylation can be used to investigate other highly relevant PTMs in blood samples such as phosphorylation and glycosylation. This study provides insights into the regulation of ADP-ribosylated proteins by writers and erasers that are present in the blood. Understanding the functions of ADP-ribosylation of extracellular proteins in disease will help to unravel the mechanisms underlying SIRS and sepsis, two of the major health threats today. Using these findings to further characterize dynamics of plasma protein ADP-ribosylation will give rise to a vast array of new research possibilities and diagnostic tools.

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7. FIGURES

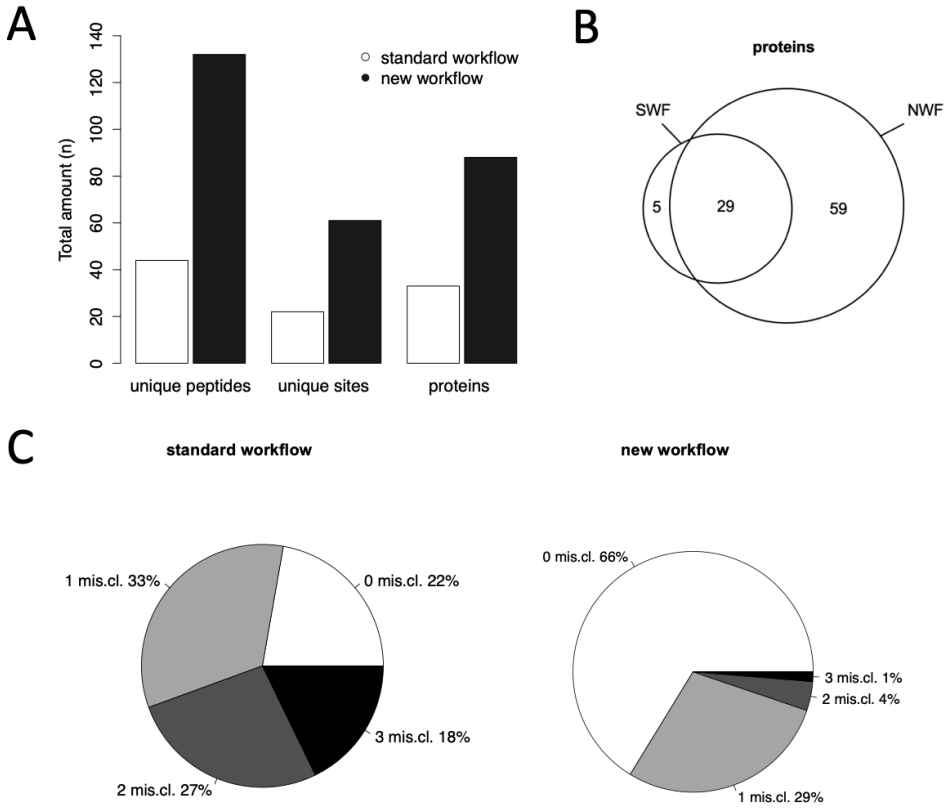


Figure 1: Comparison of the standard and new workflow using HeLa H_2O_2 treated cell lysates.
A: Comparison of number of unique peptides, unique modification sites (>95% localization confidence) and proteins identified in HeLa H_2O_2-treated cells via LC-MS/MS analyses when samples were prepare using either the standard and new workflow. Combined HCD and EThcD data is shown. B: Venn diagrams showing the overlap of ADP-ribosylated proteins that were identified in either the standard or new workflow. C: Comparison of the amount of missed cleavages in peptides from HeLa H_2O_2-treated cell lysates prepared for MS analysis using the standard (left panel) or new workflow (right panel).

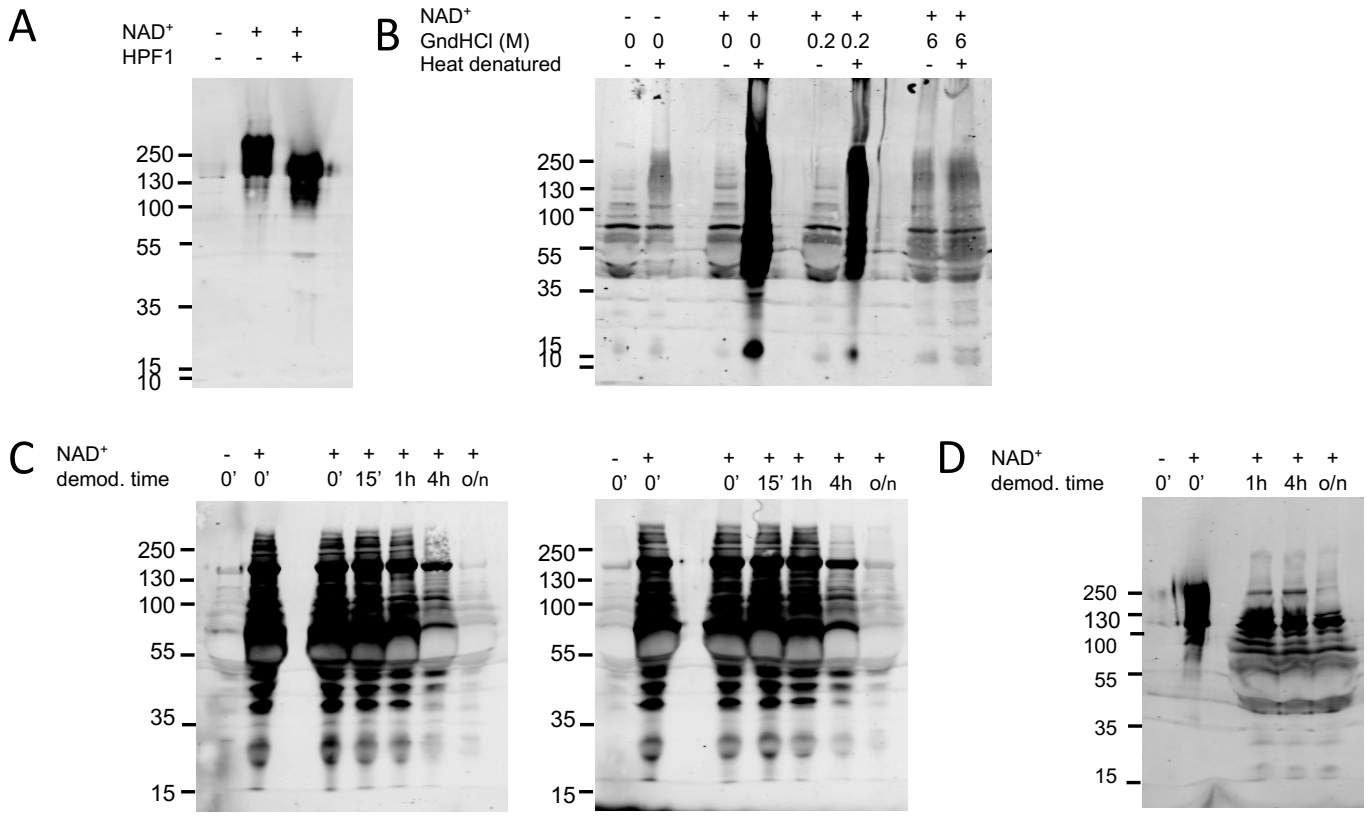


Figure 2: Inducing ADP-ribosylation via heat-denaturing and assessing demodification potential *ex vivo*.
A: Western blot analysis of auto-modified ARTD1 (Trevigen), with and without 5 µM NAD^+, activated DNA and HPF1 using the Cell Signaling anti-ADPr-antibody. B: Western blot analysis of heat-denatured (95 °C, 10 min), GndHCl-denatured and native porcine plasma using the using the Cell Signaling anti-ADPr-antibody. C: To determine how stable ADPr-modifications were in plasma samples, porcine plasma samples were ADP-ribosylated *ex vivo* via incubation with ARTC1 expressing DC27.10 cells and NAD^+. The cells were removed and the plasma incubated for 0 min, 15 min, 1 hour, 4 hours and overnight (16 h) at 37 °C. Western blot analysis of using the Cell Signaling anti-ADPr-antibody was then used to determine if ADP-ribosylation levels decreased during post-modification incubation (left panel). To determine if the observed changes were enzymatically driven, 100 µM cAMP was added to the samples after removing the cells and the samples incubated as described above (right panel) before incubation. D: ARTD1 was auto-modified as described above and then porcine plasma from healthy pigs was added these samples and incubated for 1h, 4hrs, or overnight at 37°C to assess whether auto-modified ARTD1 could also be demodified by plasma. Western blot analysis with an anti-pan-ADPr-antibody (CST) was used to assess this.

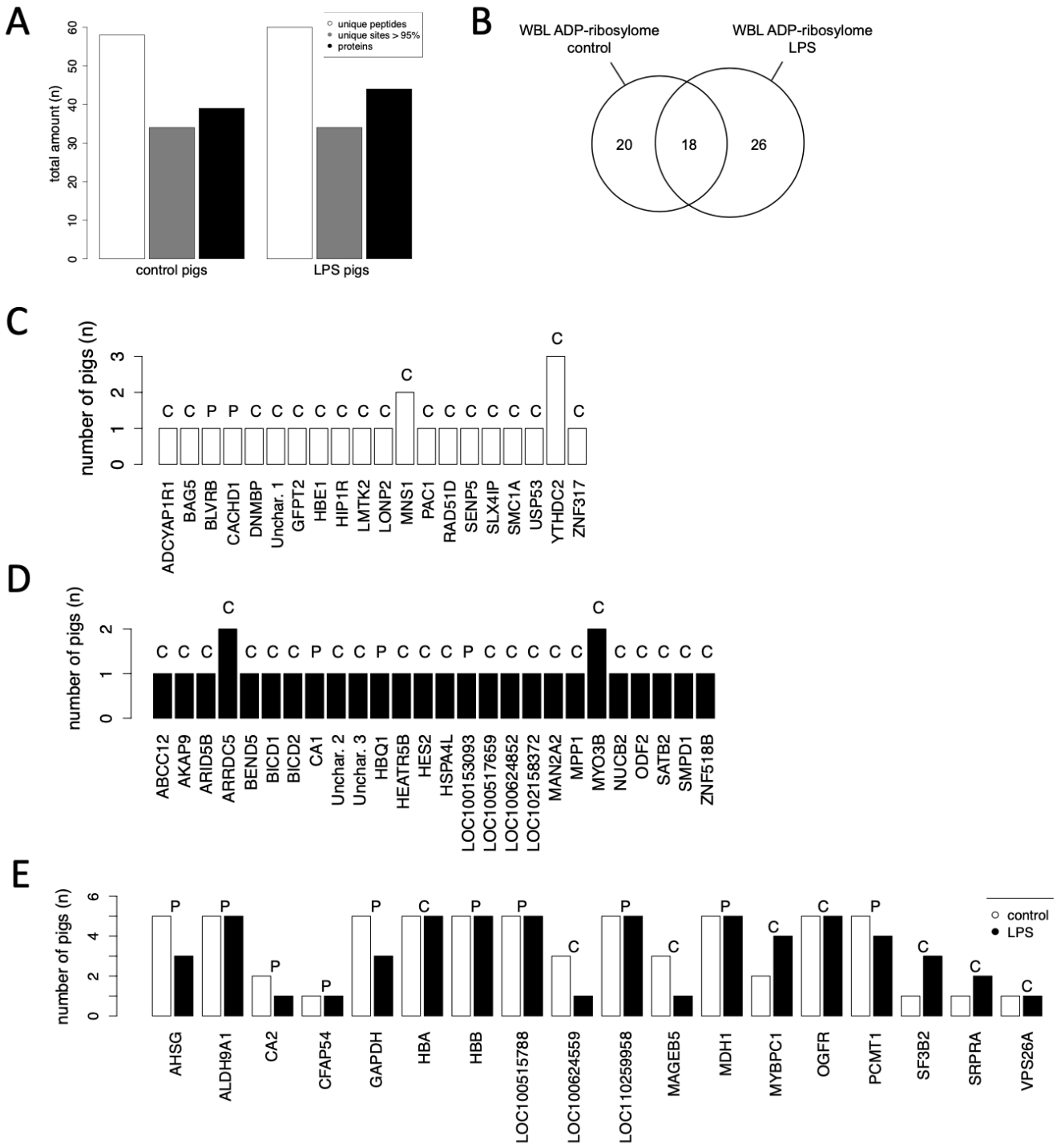


Figure 3: The *in vivo* WBL ADP-ribosylome identified in healthy and LPS-treated pigs.
A: Overview of unique ADP-ribosylated peptides, unique modification sites (> 95% localization confidence) and proteins found in the WBL ADP-ribosylome of control and LPS-treated pigs. B: Venn diagrams showing the overlap of ADP-ribosylated proteins identified in the WBL of healthy and LPS-treated pigs. C: Overview of unique ADP-ribosylated proteins found in control pigs only. D: Overview of unique ADP-ribosylated proteins found in LPS-treated pigs only. E: Overview of the unique ADP-ribosylated proteins identified in both control and LPS-treated pigs. "C" denotes proteins belonging to the cellular fraction of the blood and "P" those belonging to the plasma. Significant differences were not identified due to small sample sizes for panels C-E.

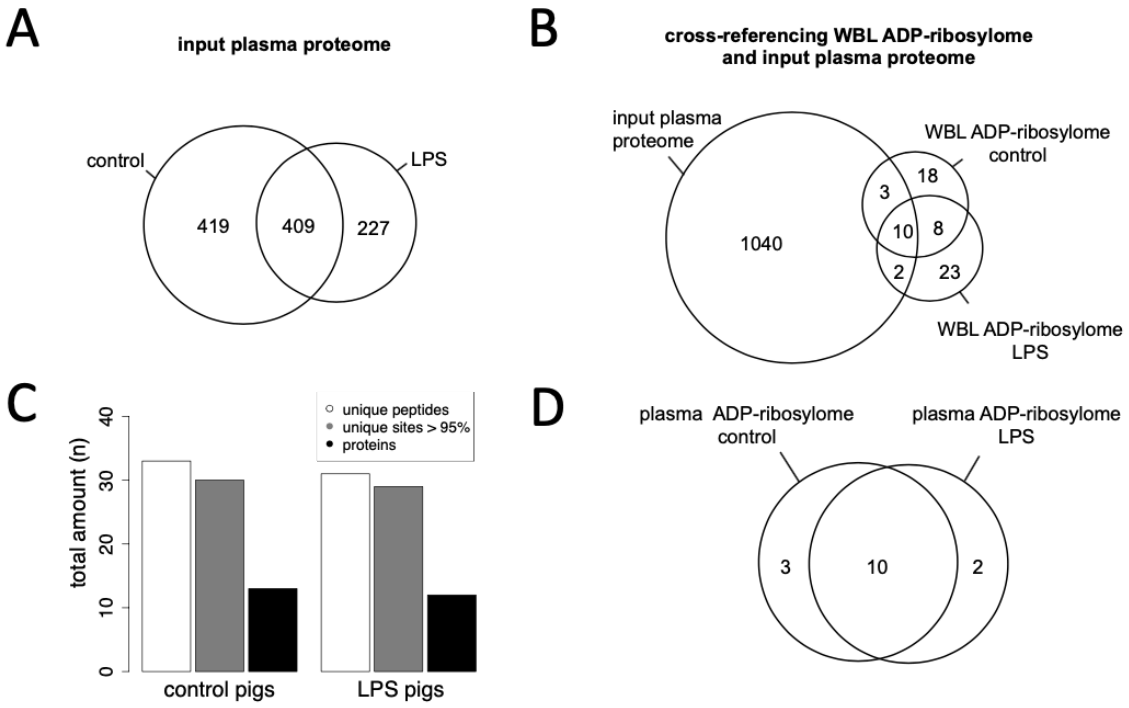


Figure 4: The *in vivo* plasma ADP-ribosylome identified in healthy and LPS-treated pigs.
A: Venn diagram showing the overlap of proteins found in the plasma samples of control and LPS-treated pigs. B: The plasma ADP-ribosylome of control and LPS-treated pigs was determined by cross-referencing the WBL ADP-ribosylome of both groups with the reference plasma proteome (generated by combining the plasma proteomes of both groups). C: Overview of unique ADP-ribosylated peptides, unique modification sites (> 95% localization confidence) and proteins found in the plasma ADP-ribosylome of control and LPS-treated pigs. D: Venn diagram showing the overlap of ADP-ribosylated plasma proteins identified in control and LPS-treated pigs.

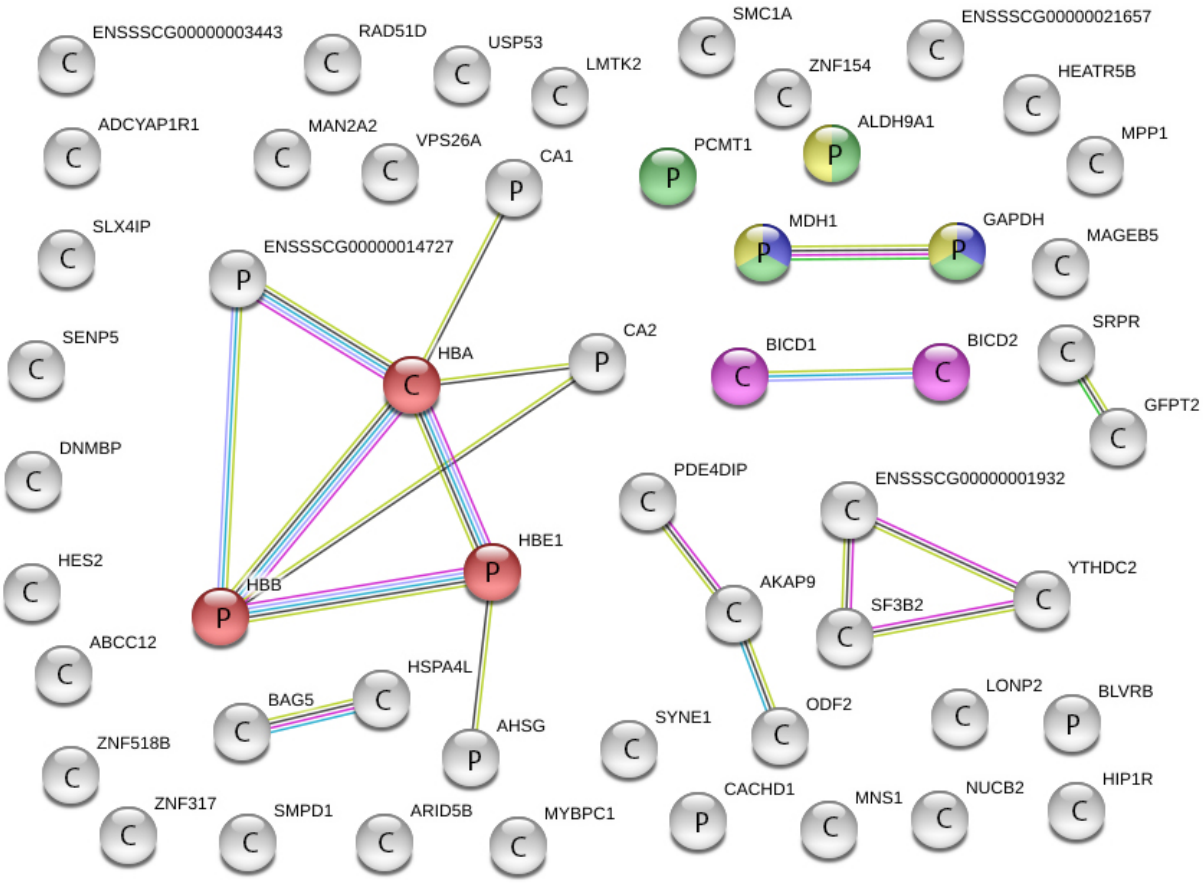
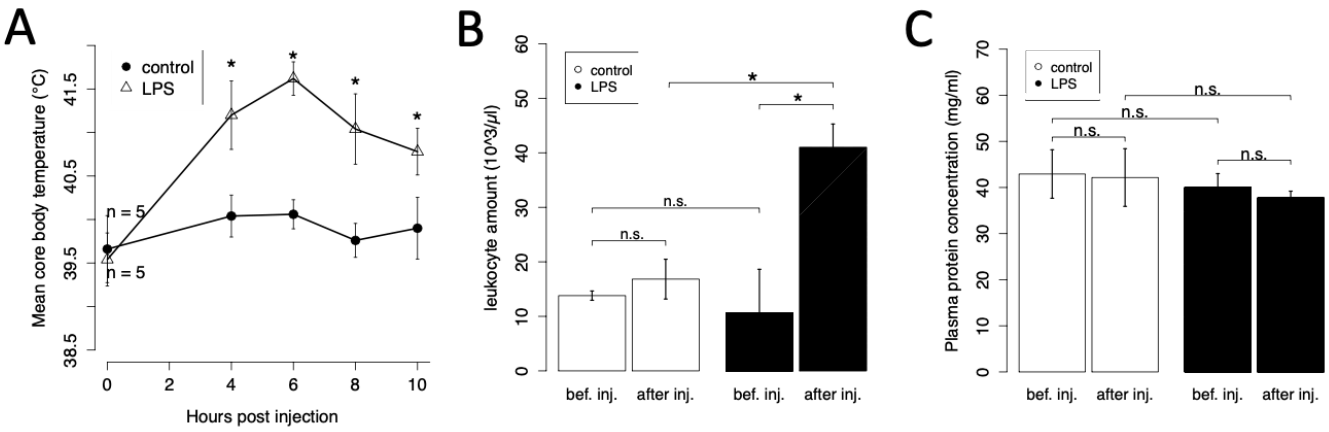
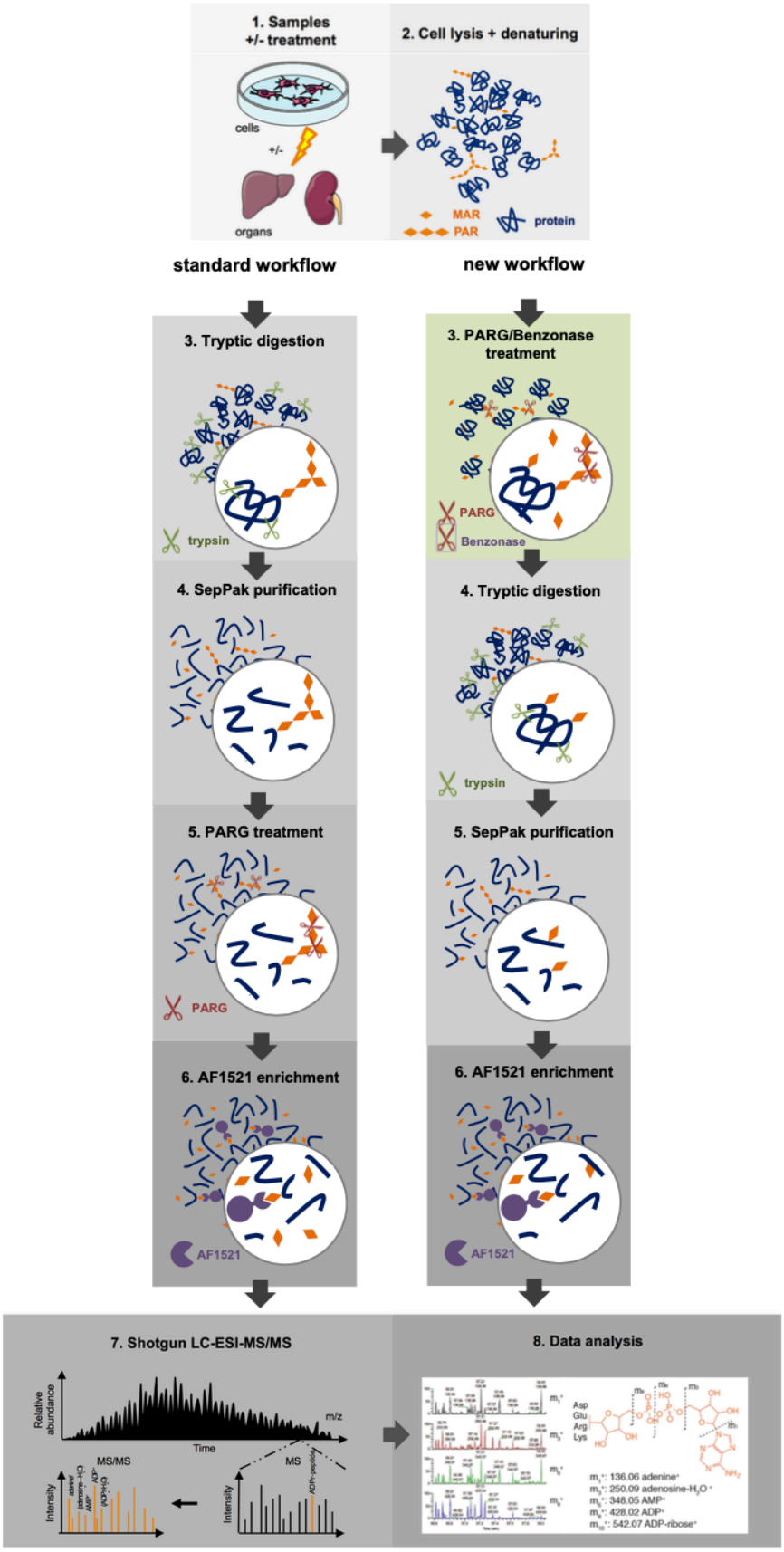


Figure 5: Functional protein network analyses (STRING) of ADP-ribosylated proteins identified in healthy and LPS-treated pigs.
STRING analysis of all ADP-ribosylated proteins identified here revealed network and functional enrichments for oxygen transport (red), nicotinamide nucleotide metabolic processes (blue), microtubule associated proteins (pink), organonitrogen compound metabolic process (green), and oxidation-reduction processes (yellow). "C" denotes proteins belonging to the cellular fraction of the blood and "P" those belonging to the plasma.

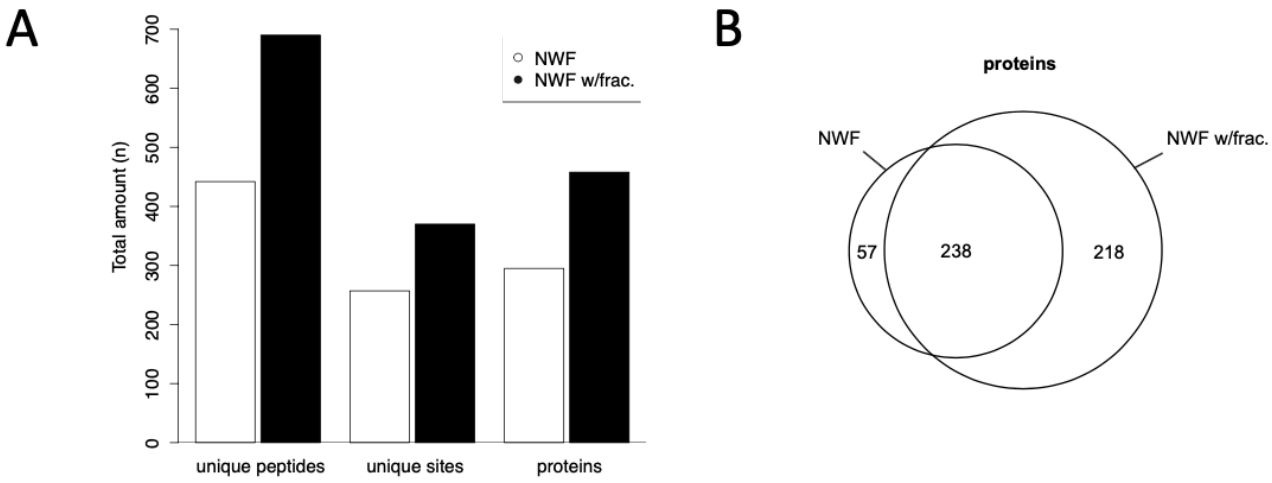


Supplementary Figure 1: Specific and significant increases in core body temperatures and leukocyte concentrations were observed after LPS injections.

A: Mean core body temperature (°C) of pigs ± standard deviation after NaCl (control group) or LPS (treatment group) injections at indicated timepoints during the LPS trial. B: Mean leukocyte amounts (x $10^3/\mu l$) ± standard deviation before and after NaCl (control group) or LPS (treatment group) injection during the LPS trial. C: Mean plasma protein concentration ± standard deviation before and after injection during the LPS trial. Significant differences ($p < 0.05$) are labeled with an asterisk (*) while non-significant differences are labeled "n.s.".

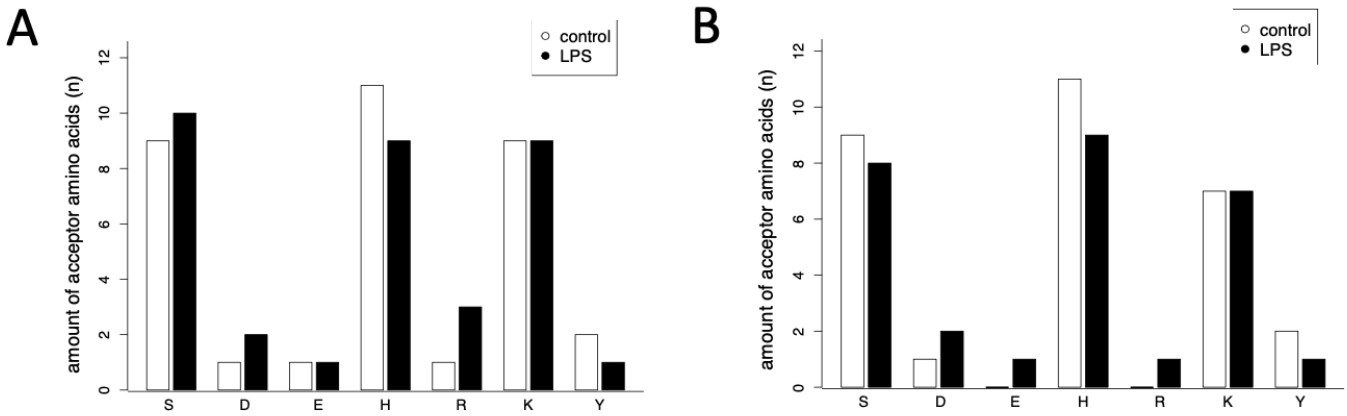


Supplementary Figure 2: Overview of standard workflow and new workflow for MS sample preparation. The standard workflow includes tryptic digestion, C18-SepPak peptide purification/clean-up, PARG-based PAR chain digestion, Af1521-based ADPr-modified peptide enrichment and a final pre-MS C18 stage-tip clean-up (left column). For the new workflow, we moved the PARG/Benzonase forward to the first step of the sample preparation protocol, this was done to optimize tryptic digestions and eliminate free ADP-ribose from the samples prior to Af1521-based ADPr-modified peptide enrichment (right column).

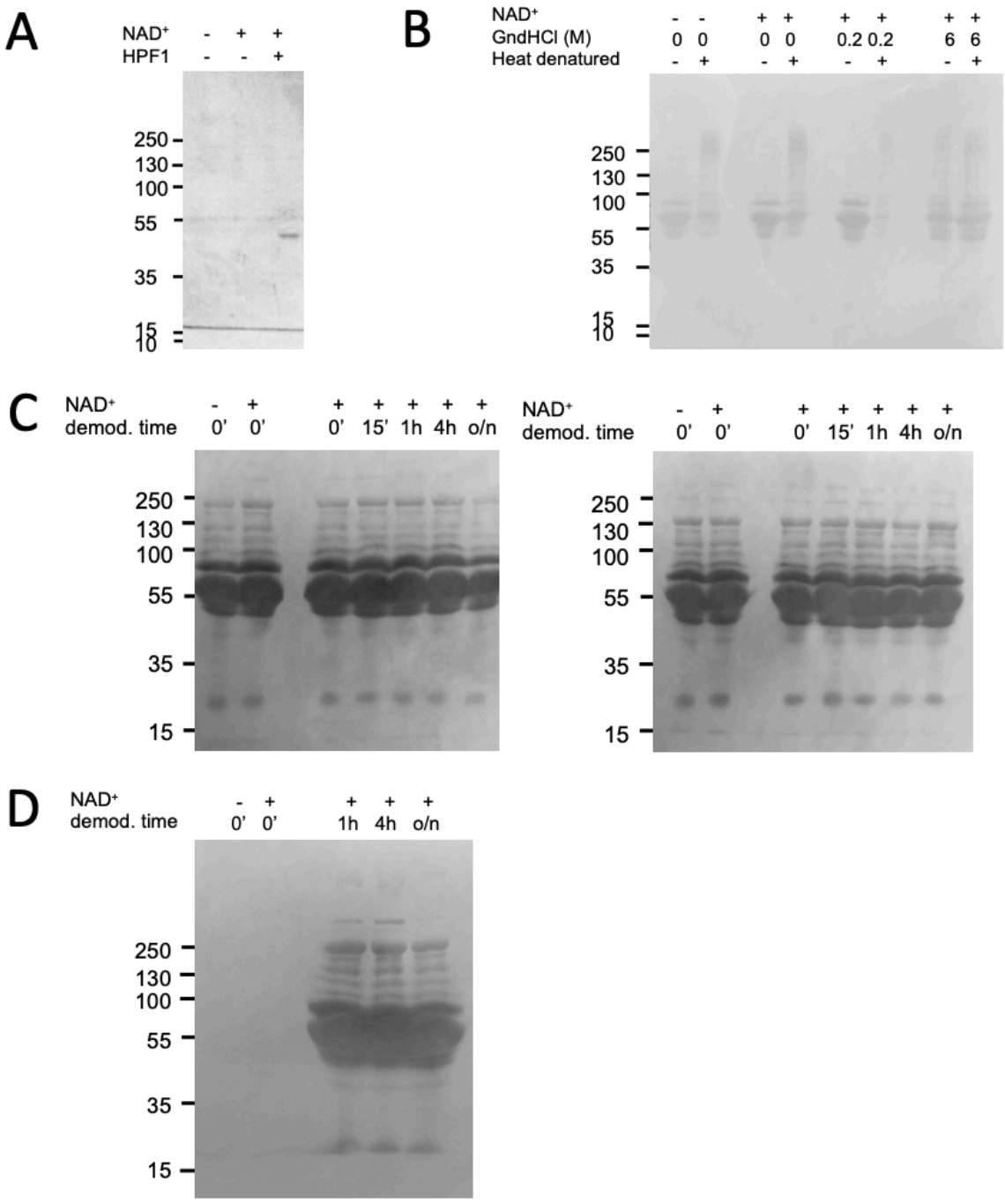


Supplementary Figure 3: Comparison of the new workflow with and without LpH/HpH fractionation using HeLa H_2O_2-treated cell lysate.

A: Comparison of number of unique peptides, unique modification sites (>95% localization confidence) and proteins identified in HeLa H_2O_2 treated cells when preparing samples for LC-MS/MS using the new workflow with and without fractionation. Combined HCD and EThcD data are shown. B: Venn diagrams showing the overlap of ADP-ribosylated proteins that were identified with the new workflow with and without fractionation.



Supplementary Figure 4: Modification site distribution of the WBL and plasma protein ADP-ribosylome.
A: Overview of the acceptor amino acids of unique sites > 95% in the WBL ADP-ribosylome. B: Overview of the acceptor amino acids of unique sites > 95% in the plasma ADP-ribosylome.



Supplementary Figure 5: Protein loading control via Ponceau staining for WB analyses (Figure 2).
A: Ponceau stain of auto-modified ARTD1 (Trevigen), with and without NAD^+, activated DNA and HPF1. B: Ponceau stain of heat-denatured (95 °C, 10 min) and non-heat-denatured porcine plasma. Samples were incubated overnight at 37 °C ± NAD^+, 0.2M or 6M GndHCl as indicated. C: Ponceau stain of the *ex vivo* induced plasma ADP-ribosylation samples presented in Figure 2 C; left panel are the samples without cAMP and the right panel samples with cAMP. D: Ponceau stain of the auto-modified ARTD1 and then plasma incubated samples presented in Figure 2D.

8. TABLES

Table 1: Experimental groups, animal experiment number, ear tag number, gender, weight and treatments of the pigs in the LPS trial.

Group	Ear tag no.	Gender	Weight (kg)	Treatment
control	1304	F	9.52	NaCl
	1296	M	10.62	NaCl
	1297	M	10.82	NaCl
	1295	F	11.14	NaCl
	1294	M	12.06	NaCl
LPS	1300	M	10.48	LPS
	1303	F	10.8	LPS
	1305	F	10.86	LPS
	1291	M	10.9	LPS
	1301	M	11.2	LPS

Table 2: detailed information on peptides, modification sites and proteins identified during the MS workflow comparison.

prot_acc	prot_desc	gene_name	PEP_ADPr_site	workflow	pep_score	pep_expect	pep_var_mod_conf	pep_var_mod	pep_start	pep_end
Q9NYF8	Bcl-2-associated transcription factor 1	BCLAF1	EYSGFAGVSRPR_E1	SWF	42.26	0.00035	87.57%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	785	796
Q9NYF8	Bcl-2-associated transcription factor 1	BCLAF1	SFATASHR_S1	SWF	31.78	0.013	100%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	422	429
Q9NYF8	Bcl-2-associated transcription factor 1	BCLAF1	EYSGFAGVSRPR_S3	SWF	21.44	0.0097	83.37%	ADP-Ribosyl-EThcD (SRDEKY) (DEKRSY)	785	796
A0A0A0MRH8	Chromodomain-helicase-DNA-binding protein 1-like	CHD1L	SAVLHSQSSSSSSR_S1	SWF	40.38	0.00016	98.81%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	599	612
Q14011	Cold-inducible RNA-binding protein	CIRBP	SGGYGGSR_S1	SWF	24.05	0.04	95.02%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	132	139
Q9BTC0	Death-inducer obliterator 1	DIDO1	RPWLSATPSSGASAAR_R1	SWF	32.35	0.00093	97.74%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	597	612
Q9BTC0	Death-inducer obliterator 1	DIDO1	RPWLSATPSSGASAAR_S5	SWF	26.18	0.0054	94.53%	ADP-Ribosyl-EThcD (SRDEKY) (DEKRSY)	597	612
P39748	Flap endonuclease 1	FEN1	VTGSLSSAK_S4	SWF	22.19	0.028	53.30%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	346	354
Q5TEC6;P68431;Q71DI3;Q16695	Histone H3;Histone H3.1;Histone H3.2;Histone H3.1t	HIST2H3PS2;HIST1H3A;HIST2H3A;HIST3H3	SAPATGGVK_S1	SWF	38.49	0.0023	100%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	29	37
P05114	Non-histone chromosomal protein HMG-14	HMGN1	KVSSAEGAAKEEPK_K1	SWF	74.17	1.70E-07	99.30%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	5	18
P05114	Non-histone chromosomal protein HMG-14	HMGN1	KVSSAEGAAKEEPK_S3	SWF	41.7	0.00013	57.73%	ADP-Ribosyl-EThcD (SRDEKY) (DEKRSY)	5	18
P05204	Non-histone chromosomal protein HMG-17	HMGN2	LSAKPAPPKPEPKPK_K4	SWF	24.95	0.0046	49.02%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	28	42
P05204	Non-histone chromosomal protein HMG-17	HMGN2	LSAKPAPPKPEPKPK_S2	SWF	28.48	0.0021	84.64%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	28	42
Q13151	Heterogeneous nuclear ribonucleoprotein A0	HNRNPA0	SGGGGGGGGSSWGGR_S1	SWF	79.36	3.60E-08	100.00%	ADP-Ribosyl-EThcD (SRDEKY) (DEKRSY)	270	284
P09651	Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	NQGGYGGSSSSSSYGSGR_Y5	SWF	53.67	9.30E-06	99.18%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	353	370
P09651	Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	SGSGNFGGGR_S1	SWF	31.29	0.0021	84.74%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	197	206
P09651	Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	SSGPYGGGGQYFAKPR_S1	SWF	52.3	1.20E-05	60.63%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	337	352
P09651	Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	SSGPYGGGGQYFAKPR_S2	SWF	43.07	9.10E-05	46.04%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	337	352
P09651	Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	NQGGYGGSSSSSSYGSGR_S11	SWF	43.17	8.90E-05	70.50%	ADP-Ribosyl-EThcD (SRDEKY) (DEKRSY)	353	370
P22626	Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	SGNFGGSR_S1	SWF	32.74	0.0058	100%	ADP-Ribosyl-EThcD (SRDEKY) (DEKRSY)	318	325
P51991	Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	SSGSPYGGGYGSGGGSGGYGSR_S4	SWF	80.55	2.80E-08	48.43%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	355	376
Q9BUJ2	Heterogeneous nuclear ribonucleoprotein U-like protein 1	HNRNPUL1	SGGGGYSQNR_S1	SWF	23.2	0.0067	100%	ADP-Ribosyl-EThcD (SRDEKY) (DEKRSY)	662	671
Q07666	KH domain-containing RNA-binding signal transduction-associated protein 1	KHDRBS1	SGSMDPSGAHPSVR_D4	SWF	44.65	6.50E-05	57.08%	Oxidation (M); ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	18	31
Q07666	KH domain-containing RNA-binding signal transduction-associated protein 1	KHDRBS1	SGSMDPSGAHPSVR_S1	SWF	78.96	6.80E-08	99.48%	Oxidation (M); ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	18	31
Q07666	KH domain-containing RNA-binding signal transduction-associated protein 1	KHDRBS1	SGSMDPSGAHPSVR_S3	SWF	39.49	0.00032	48.13%	Oxidation (M); ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	18	31
P02545	Prelamin-A/C	LMNA	SGAQASSTPLSPTR_S1	SWF	39.78	0.00022	98.77%	ADP-Ribosyl-EThcD (SRDEKY) (DEKRSY)	12	25
Q9Y6R4	Mitogen-activated protein kinase kinase kinase 4	MAP3K4	STQRAPR_S1	SWF	29.98	0.037	96.85%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	1395	1401
P46013	Antigen KI-67	MKI67	SGNLPSKR_S1	SWF	29.44	0.019	98.81%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	621	628
Q9BQG0	Myb-binding protein 1A	MYBBP1A	SPSLLQSGAK_S1	SWF	22.36	0.022	87.05%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	1308	1317
Q14978	Nucleolar and coiled-body phosphoprotein 1	NOLC1	SLGTQPPKK_S1	SWF	27.05	0.0041	100%	ADP-Ribosyl-EThcD (SRDEKY) (DEKRSY)	303	311
Q14978	Nucleolar and coiled-body phosphoprotein 1	NOLC1	VAGGAAPSKPASAK_S12	SWF	29.13	0.0019	88.93%	ADP-Ribosyl-EThcD (SRDEKY) (DEKRSY)	497	510
Q8TEM1	Nuclear pore membrane glycoprotein 210	NUP210	DSEADRFSDSHNALR_R6	SWF	33.38	0.00074	40.73%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	164	178
Q9BXS6	Nucleolar and spindle-associated protein 1	NUSAP1	SAHVTVSGGTPK_S1	SWF	27.67	0.0025	97.64%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	305	316
P09874	Poly [ADP-ribose] polymerase 1	PARP1	EEGINKSEK_E2	SWF	21.9	0.0095	63.68%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	513	521
P09874	Poly [ADP-ribose] polymerase 1	PARP1	EEGINKSEK_S7	SWF	38.69	0.0047	75.52%	ADP-Ribosyl-EThcD (SRDEKY) (DEKRSY)	513	521
P09874	Poly [ADP-ribose] polymerase 1	PARP1	SKGQVKEEGINK_K2	SWF	34.05	0.0025	49.96%	ADP-Ribosyl-EThcD (SRDEKY) (DEKRSY)	507	518
P30101	Protein disulfide-isomerase A3	PDIA3	RLAPEYEAAATR_R1	SWF	74.19	5.10E-07	100.00%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	62	73
Q8NEY8	Periphilin-1	PPHLN1	SYSFHQSQHR_Y2	SWF	22.56	0.013	45.59%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	161	170
Q8NEY8	Periphilin-1	PPHLN1	SYSFHQSQHR_S1	SWF	26.5	0.0033	74.08%	ADP-Ribosyl-EThcD (SRDEKY) (DEKRSY)	161	170
P62136	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit	PPP1CA	YGQFSGLNPGGRPITPPR_Y1	SWF	47.43	3.60E-05	99.79%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	306	323
P98179	RNA-binding protein 3	RBM3	NQGGYDRYSGGNYR_D6	SWF	20.07	0.013	43.56%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	139	152
P38159	RNA-binding motif protein X chromosome	RBMX	SAPSGPVR_S1	SWF	32.25	0.013	99.24%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	165	172
P38159	RNA-binding motif protein X chromosome	RBMX	SDLYSSGR_D2	SWF	21.48	0.021	47.78%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	332	339
P38159	RNA-binding motif protein X chromosome	RBMX	SDLYSSGR_S1	SWF	31.42	0.0037	84.05%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	332	339
P38159	RNA-binding motif protein X chromosome	RBMX	VEQATKPSFESGR_S11	SWF	38.08	0.0013	78.03%	ADP-Ribosyl-EThcD (SRDEKY) (DEKRSY)	81	93
P61247	40S ribosomal protein S3a	RPS3A	KTSYAQHQQVR_K1	SWF	37.07	0.00033	72.94%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	152	162
P61247	40S ribosomal protein S3a	RPS3A	KTSYAQHQQVR_Y4	SWF	20.91	0.011	81.73%	ADP-Ribosyl-EThcD (SRDEKY) (DEKRSY)	152	162
Q68D10	Protein SPT2 homolog	SPTY2D1	GPGRPVSSPHELR_R4	SWF	23.49	0.03	67.43%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	464	476
Q68D10	Protein SPT2 homolog	SPTY2D1	GPGRPVSSPHELR_S7	SWF	32.7	0.0019	86.13%	ADP-Ribosyl-EThcD (SRDEKY) (DEKRSY)	464	476
Q92804	TATA-binding protein-associated factor 2N	TAF15	SGGGYGGDR_S1	SWF	30.7	0.0022	99.62%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	423	431
Q92804	TATA-binding protein-associated factor 2N	TAF15	SGGYGGDR_S1	SWF	26.77	0.041	97.74%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	546	553
P11388	DNA topoisomerase 2-alpha	TOP2A	RDPALNSGVSQKPDPAK_D14	SWF	29.65	0.0032	58.64%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	1443	1459
P11388	DNA topoisomerase 2-alpha	TOP2A	RDPALNSGVSQKPDPAK_S7	SWF	33.07	0.00079	97.78%	ADP-Ribosyl-EThcD (SRDEKY) (DEKRSY)	1443	1459
Q8WZ42	Titin	TTN	ISLGARVVLTR_R6	SWF	22	0.01	94.87%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	12630	12640
O96028	Histone-lysine N-methyltransferase NSD2	WHSC1	LCSSAETLESHPDIGK_S3	SWF	23.05	0.0069	71.07%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	405	420
P25490	Transcriptional repressor protein YY1	YY1	KSYLSGGAGAAGGGGADPGNK_S5	SWF	69.09	4.90E-07	93.88%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	183	203
P25490	Transcriptional repressor protein YY1	YY1	SYLSGGAGAAGGGGADPGNK_S4	SWF	37.81	0.00028	77.86%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	184	203
P25490	Transcriptional repressor protein YY1	YY1	SYLSGGAGAAGGGGADPGNKK_S4	SWF	34.19	0.00062	24.89%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	184	204
P25490	Transcriptional repressor protein YY1	YY1	SYLSGGAGAAGGGGADPGNKK_Y2	SWF	64.82	4.50E-06	49.56%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	184	204
Q9NR48	Histone-lysine N-methyltransferase ASH1L	ASH1L	STAPSLALLADSEKPSHK_S1	NWF	70.05	2.70E-07	99.86%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	785	802
Q9NR48	Histone-lysine N-methyltransferase ASH1L	ASH1L	STAPSLALLADSEKPSHK_S5	NWF	30.11	0.0027	49.79%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	785	802
Q9UIG0	Tyrosine-protein kinase BAZ1B	BAZ1B	SLSGSPLK_S1	NWF	23.15	0.047	81.36%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	345	352
Q9NYF8	Bcl-2-associated transcription factor 1	BCLAF1	EYSGFAGVSRPR_E1	NWF	60.49	2.00E-05	91.22%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	785	796
Q9NYF8	Bcl-2-associated transcription factor 1	BCLAF1	EYSGFAGVSRPR_S3	NWF	38.73	0.00023	93.38%	ADP-Ribosyl-EThcD (SRDEKY) (DEKRSY)	785	796
Q9NYF8	Bcl-2-associated transcription factor 1	BCLAF1	SFATASHR_S1	NWF	42.19	0.00012	100%	ADP-Ribosyl-EThcD (SRDEKY) (DEKRSY)	422	429
Q9NYF8	Bcl-2-associated transcription factor 1	BCLAF1	SVLADQGK_S1	NWF	24.38	0.036	97.62%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	414	421

Table 2: detailed information on peptides, modification sites and proteins identified during the MS workflow comparison (continued).

prot_acc	prot_desc	gene_name	PEP_ADPr_site	workflow	pep_score	pep_expect	pep_var_mod_conf	pep_var_mod	pep_start	pep_end
P54132	Bloom syndrome protein	BLM	SSSIIGSSSASHTSQATSGANSK_S3	NWF	71.38	2.00E-07	33.29%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	1373	1395
Q7L1Q6	Basic leucine zipper and W2 domain-containing protein 1	BZW1	QQKPTLSGQR_K3	NWF	25.31	0.0055	100%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	6	15
Q7L1Q6	Basic leucine zipper and W2 domain-containing protein 1	BZW1	QQKPTLSGQR_S7	NWF	22.9	0.032	93.48%	ADP-Ribosyl-EThcD (SRDEKY) (DEKRSY)	6	15
Q8NDD1	Uncharacterized protein C1orf131	C1orf131	SYVNYK_S1	NWF	23.78	0.025	84.39%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	207	212
Q9NWY4	UPF0609 protein C4orf27	C4orf27	TFHGAGLVVPVDKNDVGYR_R19	NWF	21.89	0.0088	33.94%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	221	239
Q9NWY4	UPF0609 protein C4orf27	C4orf27	TFHGAGLVVPVDKNDVGYR_Y18	NWF	26.45	0.0033	60.00%	ADP-Ribosyl-EThcD (SRDEKY) (DEKRSY)	221	239
P45973	Chromobox protein homolog 5	CBX5	SNFSNSADDIK_S1	NWF	40.89	0.00015	82.75%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	92	102
Q9H6F5	Coiled-coil domain-containing protein 86	CCDC86	RFSQMLQDKPLR_R1	NWF	31.05	0.0058	79.44%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	253	264
Q9H6F5	Coiled-coil domain-containing protein 86	CCDC86	RFSQMLQDKPLR_S3	NWF	50.35	1.90E-05	99.00%	ADP-Ribosyl-EThcD (SRDEKY) (DEKRSY)	253	264
Q7Z7K6-3	Isoform 3 of Centromere protein V	CENPV	SGASAAPAASAAAALAPSATR_S10	NWF	29.57	0.019	33.31%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	18	38
Q7Z7K6-3	Isoform 3 of Centromere protein V	CENPV	SGASAAPAASAAAALAPSATR_S4	NWF	21.26	0.01	34.41%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	18	38
Q7Z7K6	Centromere protein V	CENPV	SGASGASAAPAASAAAALAPSATR_S13	NWF	34.45	0.001	24.99%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	18	41
Q7Z7K6	Centromere protein V	CENPV	SGASGASAAPAASAAAALAPSATR_S7	NWF	36.44	0.00038	32.87%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	18	41
Q14011	Cold-inducible RNA-binding protein	CIRBP	SGGYGGSR_S1	NWF	33.4	0.03	98.88%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	132	139
Q14011	Cold-inducible RNA-binding protein	CIRBP	SQSGGYSDR_S1	NWF	23.52	0.0066	60.83%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	146	154
Q8N684	Cleavage and polyadenylation specificity factor subunit 7	CPSF7	SYSVGASGSSSR_Y2	NWF	29.05	0.0019	39.79%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	407	418
Q9H8H2	Probable ATP-dependent RNA helicase DDX31	DDX31	SHAVGPQEIR_S1	NWF	43.72	8.10E-05	99.93%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	678	687
Q08211	ATP-dependent RNA helicase A	DHX9	YDNGSGYR_Y1	NWF	30.57	0.019	87.32%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	1167	1174
Q9BTC0	Death-inducer obliterator 1	DIDO1	RPWLSATPSSGASAAR_R1	NWF	45.95	9.80E-05	99.83%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	597	612
Q9BTC0	Death-inducer obliterator 1	DIDO1	SSFANVAAATPAIK_S2	NWF	32.81	0.0017	49.99%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	571	584
Q9UNQ2	Probable dimethyladenosine transferase	DIMT1	SAGGLMFNTGIGQHILK_S1	NWF	28.39	0.0022	100%	Oxidation (M); ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	24	40
O43768	Alpha-endosulfine	ENSA	SSLVTSK_S2	NWF	25.9	0.046	64.32%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	108	114
Q01780	Exosome component 10	EXOSC10	SMSFPTGK_S1	NWF	26.93	0.0052	94.68%	Oxidation (M); ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	866	873
Q9BTL3	RNMT-activating mini protein	FAM103A1	SWGNNYPQHR_S1	NWF	32.49	0.00094	99.87%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	86	95
Q5HYJ3	Protein FAM76B	FAM76B	SSATIQNETPK_S2	NWF	24.5	0.005	27.87%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	207	217
P39748	Flap endonuclease 1	FEN1	VTGSLSSAK_S7	NWF	25.35	0.0042	44.28%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	346	354
P39748	Flap endonuclease 1	FEN1	VTGSLSSAKR_S4	NWF	30.99	0.0022	94.43%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	346	355
P39748-2	Isoform FENMIT of Flap endonuclease 1	FEN1	VTGSLSSAKR_S7	NWF	51.51	6.00E-04	95.95%	ADP-Ribosyl-EThcD (SRDEKY) (DEKRSY)	282	291
P35637	RNA-binding protein FUS	FUS	SSGGYEPR_S1	NWF	60.63	6.30E-05	94.39%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	235	242
P84243	Histone H3.3	H3F3A	SAPSTGGVK_S1	NWF	27.82	0.018	97.36%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	29	37
P68431;Q5TEC6;Q16695	Histone H3.1;Histone H3;Histone H3.1t	HIST1H3A;HIST2H3PS2;HIST3H3	SAPATGGVK_S1	NWF	21.52	0.023	100%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	29	37
P17096	High mobility group protein HMG-I/HMG-Y	HMGA1	KQPPVSPGTALVGSQKEPSEVPTPK_K1	NWF	26.07	0.0036	90.03%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	31	55
P17096;A6NN90	High mobility group protein HMG-I/HMG-Y;Uncharacterized protein C2orf81	HMGA1;C2orf81	SSQPLASK_S1	NWF	29.91	0.034	84.86%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	8	15
P17096;A6NN90	High mobility group protein HMG-I/HMG-Y;Uncharacterized protein C2orf81	HMGA1;C2orf81	SSQPLASK_S2	NWF	33.43	0.029	49.87%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	8	15
P05114	Non-histone chromosomal protein HMG-14	HMGN1	KVSSAEGAAKEEPK_K1	NWF	76.06	6.80E-06	99.09%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	5	18
P05114	Non-histone chromosomal protein HMG-14	HMGN1	KVSSAEGAAKEEPK_S3	NWF	91.49	1.80E-08	97.78%	ADP-Ribosyl-EThcD (SRDEKY) (DEKRSY)	5	18
P05204	Non-histone chromosomal protein HMG-17	HMGN2	LSAKPAPPKPEPKPK_K4	NWF	27.54	0.0026	48.62%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	28	42
P05204	Non-histone chromosomal protein HMG-17	HMGN2	LSAKPAPPKPEPKPK_S2	NWF	48.54	2.80E-05	97.38%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	28	42
Q13151	Heterogeneous nuclear ribonucleoprotein A0	HNRNPA0	SGGGGGGGGSSWGGR_S1	NWF	85.34	2.30E-08	100.00%	ADP-Ribosyl-EThcD (SRDEKY) (DEKRSY)	270	284
P09651	Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	NQGGYGGSSSSSSYGSGR_S11	NWF	63.26	1.20E-06	25.99%	ADP-Ribosyl-EThcD (SRDEKY) (DEKRSY)	353	370
P09651	Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	NQGGYGGSSSSSSYGSGR_S13	NWF	26.12	0.0036	42.41%	ADP-Ribosyl-EThcD (SRDEKY) (DEKRSY)	353	370
P09651	Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	NQGGYGGSSSSSSYGSGR_S16	NWF	70.45	2.50E-07	69.21%	ADP-Ribosyl-EThcD (SRDEKY) (DEKRSY)	353	370
P09651	Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	NQGGYGGSSSSSSYGSGR_Y5	NWF	72.21	1.70E-07	99.88%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	353	370
P09651	Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	SESPKEPEQLR_E2	NWF	20.41	0.012	31.55%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	4	14
P09651	Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	SGSGNFGGGR_S1	NWF	54.65	3.20E-05	98.73%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	197	206
P09651	Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	SKSESPKEPEQLR_K2	NWF	22.4	0.01	47.15%	Acetyl (Protein N-term); ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	2	14
P09651	Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	SSGPYGGGGQYFAKPR_S1	NWF	118.91	7.10E-12	86.39%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	337	352
P09651	Heterogeneous nuclear ribonucleoprotein A1	HNRNPA1	SSGPYGGGGQYFAKPR_S2	NWF	129.29	1.20E-12	50.00%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	337	352
P22626	Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	NMGGPYGGGNYGPGGSGGSGGYGGR_Y2	NWF	90.36	3.40E-09	99.96%	Oxidation (M); ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	326	350
P22626	Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	NMGGPYGGGNYGPGGSGGSGGYGGR_Y6	NWF	37.1	0.00033	97.29%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	326	350
P22626	Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	SGNFGGSR_S1	NWF	34.39	0.0048	100%	ADP-Ribosyl-EThcD (SRDEKY) (DEKRSY)	318	325
P51991	Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	SSGSPYGGGYGSGGGSGGYGSR_S1	NWF	63.01	1.20E-06	87.81%	ADP-Ribosyl-EThcD (SRDEKY) (DEKRSY)	355	376
P51991	Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	SSGSPYGGGYGSGGGSGGYGSR_S12	NWF	26.09	0.0036	66.65%	ADP-Ribosyl-EThcD (SRDEKY) (DEKRSY)	355	376
P51991	Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	SSGSPYGGGYGSGGGSGGYGSR_S2	NWF	125.6	1.70E-12	49.15%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	355	376
P51991	Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	SSGSPYGGGYGSGGGSGGYGSR_S4	NWF	35.72	0.00045	50.85%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	355	376
P07910	Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	SGFNSK_S1	NWF	21.74	0.046	95.75%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	171	176
P14866	Heterogeneous nuclear ribonucleoprotein L	HNRNPL	YYGGGSEGGR_Y1	NWF	28.25	0.0022	76.94%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	47	56
O43390	Heterogeneous nuclear ribonucleoprotein R	HNRNPR	STAYEDYYYHPPPR_S1	NWF	55.66	6.00E-06	90.16%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	428	441
Q00839	Heterogeneous nuclear ribonucleoprotein U	HNRNPU	SSGPTSLFAVTVAPPGAR_S6	NWF	36.64	0.00039	47.23%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	187	204
Q9BUJ2	Heterogeneous nuclear ribonucleoprotein U-like protein 1	HNRNPUL1	SGGGGYSQNR_S1	NWF	84.31	3.00E-07	100.00%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	662	671
Q1KMD3	Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	SRGQGYVGGQR_R2	NWF	43.31	0.00013	49.99%	ADP-Ribosyl-EThcD (SRDEKY) (DEKRSY)	655	665
Q12906	Interleukin enhancer-binding factor 3	ILF3	SGGNSYGSGGASYNPGSHGGYGGGSGGGSSYQGK_Y6	NWF	59.02	2.90E-06	33.02%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	816	849
Q07666	KH domain-containing RNA-binding signal transduction-associated protein 1	KHDRBS1	SGSMDPSGAHPSVR_D4	NWF	34.32	0.0013	46.62%	Oxidation (M); ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	18	31
Q07666	KH domain-containing RNA-binding signal transduction-associated protein 1	KHDRBS1	SGSMDPSGAHPSVR_S1	NWF	72.87	1.50E-07	99.56%	Oxidation (M); ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	18	31
Q07666	KH domain-containing RNA-binding signal transduction-associated protein 1	KHDRBS1	SGSMDPSGAHPSVR_S3	NWF	55.75	1.10E-05	49.05%	Oxidation (M); ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	18	31

Table 2: detailed information on peptides, modification sites and proteins identified during the MS workflow comparison (continued).

prot_acc	prot_desc	gene_name	PEP_ADPr_site	workflow	pep_score	pep_expect	pep_var_mod_conf	pep_var_mod	pep_start	pep_end
P02545	Prelamin-A/C	LMNA	SGAQASSTPLSPTR_S1	NWF	60.14	2.90E-06	99.95%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	12	25
P02545	Prelamin-A/C	LMNA	SVGGSGGGSFGDNLVTR_S1	NWF	71.12	2.20E-07	98.84%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	628	644
P02545	Prelamin-A/C	LMNA	SVGGSGGGSFGDNLVTR_S5	NWF	26.11	0.0036	48.45%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	628	644
O95243	Methyl-CpG-binding domain protein 4	MBD4	SCSGFVQSDSKR_S1	NWF	79.42	1.90E-06	98.57%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	253	264
P46013	Antigen KI-67	MKI67	SGGSGHAVAEPASPEQELDQNK_S1	NWF	94.97	1.70E-09	91.54%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	296	317
P46013	Antigen KI-67	MKI67	SGGSGHAVAEPASPEQELDQNK_S13	NWF	20.1	0.031	30.38%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	296	317
P46013	Antigen KI-67	MKI67	SGGSGHAVAEPASPEQELDQNK_S4	NWF	53.44	0.00018	49.81%	ADP-Ribosyl-EThcD (SRDEKY) (DEKRSY)	296	317
P46013	Antigen KI-67	MKI67	SGLQTDYATEK_S1	NWF	36.95	0.0015	99.65%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	264	274
P46013	Antigen KI-67	MKI67	SGNLPSKR_S1	NWF	37.81	0.0068	99.63%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	621	628
Q96NY9	Crossover junction endonuclease MUS81	MUS81	AGGSGSYWPAR_S4	NWF	25.58	0.03	80.95%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	124	134
Q9BQG0	Myb-binding protein 1A	MYBBP1A	SPSLLQSGAK_S1	NWF	28.18	0.023	75.82%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	1308	1317
Q14978	Nucleolar and coiled-body phosphoprotein 1	NOLC1	SLGTQPPKK_S1	NWF	24.89	0.0063	100%	ADP-Ribosyl-EThcD (SRDEKY) (DEKRSY)	303	311
Q14978	Nucleolar and coiled-body phosphoprotein 1	NOLC1	VAGGAAPSKPASAK_S12	NWF	37.94	0.00028	90.63%	ADP-Ribosyl-EThcD (SRDEKY) (DEKRSY)	497	510
P06748	Nucleophosmin	NPM1	SNQNGKDSKPSSTPR_S1	NWF	21.4	0.01	76.73%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	207	221
Q14980	Nuclear mitotic apparatus protein 1	NUMA1	KLGNSLLR_K1	NWF	23.77	0.044	100%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	2058	2065
Q14980	Nuclear mitotic apparatus protein 1	NUMA1	SAPASQASLR_S1	NWF	40.6	0.0018	99.81%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	1840	1849
Q8TEM1	Nuclear pore membrane glycoprotein 210	NUP210	DSEADRFSDSHNALR_R6	NWF	28.44	0.0022	35.55%	ADP-Ribosyl-EThcD (SRDEKY) (DEKRSY)	164	178
Q9BXS6	Nucleolar and spindle-associated protein 1	NUSAP1	KSAHVTVSGGTPK_K1	NWF	52.12	6.50E-05	92.31%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	304	316
Q9BXS6	Nucleolar and spindle-associated protein 1	NUSAP1	KSAHVTVSGGTPK_S8	NWF	35.14	0.00051	98.42%	ADP-Ribosyl-EThcD (SRDEKY) (DEKRSY)	304	316
Q9BXS6	Nucleolar and spindle-associated protein 1	NUSAP1	SAHVTVSGGTPK_S1	NWF	70.84	3.40E-06	100.00%	ADP-Ribosyl-EThcD (SRDEKY) (DEKRSY)	305	316
Q9BXS6	Nucleolar and spindle-associated protein 1	NUSAP1	SCGPASQSTLGLK_S1	NWF	65.25	1.10E-05	99.99%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	255	267
Q9BXS6	Nucleolar and spindle-associated protein 1	NUSAP1	SLYTDESSKPGK_S1	NWF	30.98	0.0016	89.87%	ADP-Ribosyl-EThcD (SRDEKY) (DEKRSY)	163	174
Q13415	Origin recognition complex subunit 1	ORC1	SSLHTLTK_S1	NWF	30.34	0.0094	93.78%	ADP-Ribosyl-EThcD (SRDEKY) (DEKRSY)	449	456
P07237	Protein disulfide-isomerase	P4HB	VDATEESDLAQQYGVRGYPTIK_R16	NWF	23.24	0.0066	63.13%	ADP-Ribosyl-EThcD (SRDEKY) (DEKRSY)	82	103
Q86U42	Polyadenylate-binding protein 2	PABPN1	AAAAAAAAAAGAAGGRGSGPGR_S18	NWF	31.37	0.0021	48.86%	Acetyl (Protein N-term); ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	2	23
P09874	Poly [ADP-ribose] polymerase 1	PARP1	EEGINKSEK_E1	NWF	31.11	0.011	69.35%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	513	521
P09874	Poly [ADP-ribose] polymerase 1	PARP1	EEGINKSEK_E2	NWF	28.78	0.01	63.95%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	513	521
P09874	Poly [ADP-ribose] polymerase 1	PARP1	EEGINKSEK_S7	NWF	30.87	0.045	47.87%	ADP-Ribosyl-EThcD (SRDEKY) (DEKRSY)	513	521
P09874	Poly [ADP-ribose] polymerase 1	PARP1	EEGINKSEKR_E2	NWF	20.67	0.036	49.35%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	513	522
P09874	Poly [ADP-ribose] polymerase 1	PARP1	EEGINKSEKR_S7	NWF	26.07	0.01	85.51%	ADP-Ribosyl-EThcD (SRDEKY) (DEKRSY)	513	522
P09874	Poly [ADP-ribose] polymerase 1	PARP1	GKSGAALSK_K2	NWF	39.19	0.0033	87.32%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	497	505
P09874	Poly [ADP-ribose] polymerase 1	PARP1	GKSGAALSK_S3	NWF	30.43	0.016	49.86%	ADP-Ribosyl-EThcD (SRDEKY) (DEKRSY)	497	505
P09874	Poly [ADP-ribose] polymerase 1	PARP1	GKSGAALSKK_S2	NWF	23.72	0.023	100%	2 ADP-Ribosyl-EThcD (SRDEKY) (DEKRSY)	497	506
P09874	Poly [ADP-ribose] polymerase 1	PARP1	GQVKEEGINKSEK_E12	NWF	24.9	0.0064	25.01%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	509	521
P09874	Poly [ADP-ribose] polymerase 1	PARP1	GQVKEEGINKSEK_K10	NWF	23.53	0.0068	37.65%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	509	521
P09874	Poly [ADP-ribose] polymerase 1	PARP1	GQVKEEGINKSEK_S11	NWF	25.36	0.024	45.41%	ADP-Ribosyl-EThcD (SRDEKY) (DEKRSY)	509	521
P09874	Poly [ADP-ribose] polymerase 1	PARP1	SGAALSK_S1	NWF	38.95	0.013	98.89%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	499	505
P09874	Poly [ADP-ribose] polymerase 1	PARP1	SKGQVKEEGINK_K1	NWF	60.97	4.80E-06	99.99%	2 ADP-Ribosyl-EThcD (SRDEKY) (DEKRSY)	507	518
P09874	Poly [ADP-ribose] polymerase 1	PARP1	SKGQVKEEGINK_K2	NWF	24.25	0.0059	47.52%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	507	518
P09874	Poly [ADP-ribose] polymerase 1	PARP1	SKGQVKEEGINK_S1	NWF	78.49	3.20E-07	95.30%	ADP-Ribosyl-EThcD (SRDEKY) (DEKRSY)	507	518
P09874	Poly [ADP-ribose] polymerase 1	PARP1	SKGQVKEEGINKSEK_K1	NWF	28.08	0.0043	82.05%	2 ADP-Ribosyl-EThcD (SRDEKY) (DEKRSY)	507	521
O94913	Pre-mRNA cleavage complex 2 protein Pcf11	PCF11	SGWEENK_S1	NWF	24.67	0.034	96.60%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	599	605
P22061	Protein-L-isoaspartate(D-aspartate) O-methyltransferase	PCMT1	SGGASHSELIHNLR_S1	NWF	35.08	0.00055	87.51%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	5	18
P30101	Protein disulfide-isomerase A3	PDIA3	RLAPEYEAAATR_R1	NWF	67.01	4.30E-06	100.00%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	62	73
Q9BY77	Polymerase delta-interacting protein 3	POLDIP3	SSGASVTTQPTEFK_S2	NWF	23.53	0.0062	48.27%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	405	418
Q8NEY8	Periphilin-1	PPHLN1	SVRPGASYK_S1	NWF	29.69	0.0021	95.38%	ADP-Ribosyl-EThcD (SRDEKY) (DEKRSY)	172	180
Q8NEY8	Periphilin-1	PPHLN1	SYSFHQSQHR_S1	NWF	42.98	9.30E-05	80.99%	ADP-Ribosyl-EThcD (SRDEKY) (DEKRSY)	161	170
Q8NEY8	Periphilin-1	PPHLN1	SYSFHQSQHR_S3	NWF	37.46	0.00078	42.47%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	161	170
Q8NEY8	Periphilin-1	PPHLN1	SYSFHQSQHR_Y2	NWF	24.31	0.0074	44.92%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	161	170
Q8WUA2	Peptidyl-prolyl cis-trans isomerase-like 4	PPIL4	SKYQTDLYER_K2	NWF	32.5	0.0016	46.47%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	459	468
Q8WUA2	Peptidyl-prolyl cis-trans isomerase-like 4	PPIL4	SKYQTDLYER_S1	NWF	58.25	6.30E-06	91.03%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	459	468
P62136	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit	PPP1CA	YGQFSGLNPGGRPITPPR_Y1	NWF	45.61	5.30E-05	99.62%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	306	323
P98179	RNA-binding protein 3	RBM3	NQGGYDRYSGGNYR_Y5	NWF	23.52	0.0062	30.34%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	139	152
P98179	RNA-binding protein 3	RBM3	YSGGNYR_Y1	NWF	28.73	0.0089	89.70%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	146	152
P38159	RNA-binding motif protein X chromosome	RBMX	AIKVEQATKPSFESGR_K3	NWF	54.78	7.30E-06	94.28%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	78	93
P38159	RNA-binding motif protein X chromosome	RBMX	AIKVEQATKPSFESGR_R16	NWF	52.92	6.80E-05	47.35%	ADP-Ribosyl-EThcD (SRDEKY) (DEKRSY)	78	93
P38159	RNA-binding motif protein X chromosome	RBMX	DRDYSDHPSGGSYR_D1	NWF	34.98	0.00052	75.58%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	269	282
P38159	RNA-binding motif protein X chromosome	RBMX	DYGHSSSRDDYPSR_D1	NWF	26.03	0.0036	44.33%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	245	258
P38159	RNA-binding motif protein X chromosome	RBMX	GPPPSYGGSSR_S9	NWF	20.06	0.013	45.99%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	299	309
P38159	RNA-binding motif protein X chromosome	RBMX	SAPSGPVR_S1	NWF	27.8	0.044	98.67%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	165	172
P38159	RNA-binding motif protein X chromosome	RBMX	SDLYSSGR_D2	NWF	23.71	0.0082	47.33%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	332	339
P38159	RNA-binding motif protein X chromosome	RBMX	SDLYSSGR_S1	NWF	39.68	0.00058	90.78%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	332	339
P38159	RNA-binding motif protein X chromosome	RBMX	VEQATKPSFESGR_E10	NWF	31.56	0.0052	60.68%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	81	93
P38159	RNA-binding motif protein X chromosome	RBMX	VEQATKPSFESGR_E2	NWF	27.7	0.01	52.69%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	81	93
P38159	RNA-binding motif protein X chromosome	RBMX	VEQATKPSFESGR_S11	NWF	58.1	0.00035	83.85%	ADP-Ribosyl-EThcD (SRDEKY) (DEKRSY)	81	93
P38159	RNA-binding motif protein X chromosome	RBMX	VEQATKPSFESGRR_R13	NWF	40.01	0.00044	43.74%	ADP-Ribosyl-EThcD (SRDEKY) (DEKRSY)	81	94
P38159;Q96E39	RNA-binding motif protein X chromosome;RNA binding motif protein X-linked-like-1	RBMX;RBMXL1	YDDYSSSR_Y1	NWF	42.51	1.00E-04	84.08%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	310	317

Table 2: detailed information on peptides, modification sites and proteins identified during the MS workflow comparison (continued).

prot_acc	prot_desc	gene_name	PEP_ADPr_site	workflow	pep_score	pep_expect	pep_var_mod_conf	pep_var_mod	pep_start	pep_end
P35251	Replication factor C subunit 1	RFC1	SSADKIGEVSSPK_S1	NWF	32.99	0.00081	84.90%	ADP-Ribosyl-EThcD (SRDEKY) (DEKRSY)	302	314
P35251	Replication factor C subunit 1	RFC1	SSADKIGEVSSPK_S2	NWF	47.66	0.00029	49.19%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	302	314
P83731	60S ribosomal protein L24	RPL24	VELCSFSGYK_E2	NWF	34.84	0.00054	98.29%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	3	12
P62917	60S ribosomal protein L8	RPL8	ASGNYATVISHNPETK_S2	NWF	60.14	2.30E-06	98.14%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	129	144
P62917	60S ribosomal protein L8	RPL8	ASGNYATVISHNPETK_Y5	NWF	46.41	1.00E-04	50.34%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	129	144
P61247	40S ribosomal protein S3a	RPS3A	KTSYAQHQQVR_K1	NWF	55.4	2.90E-05	97.27%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	152	162
P61247	40S ribosomal protein S3a	RPS3A	KTSYAQHQQVR_Y4	NWF	36.6	0.00037	92.58%	ADP-Ribosyl-EThcD (SRDEKY) (DEKRSY)	152	162
H0Y8L7	40S ribosomal protein S3a (Fragment)	RPS3A	TSYAQHQQVR_Y3	NWF	38.85	0.00024	50.00%	ADP-Ribosyl-EThcD (SRDEKY) (DEKRSY)	148	157
Q9NWH9	SAFB-like transcription modulator	SLTM	EVSGHSVR_E1	NWF	23.25	0.0076	82.92%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	907	914
Q9NWH9	SAFB-like transcription modulator	SLTM	GSGSGFKPFK_S2	NWF	30.24	0.0093	80.86%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	1018	1027
Q9NWH9	SAFB-like transcription modulator	SLTM	SSASGYGSR_S1	NWF	25.73	0.0043	83.55%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	922	930
Q68D10	Protein SPT2 homolog	SPTY2D1	GPGRPVSSPHELR_R4	NWF	44.1	0.00039	78.14%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	464	476
Q68D10	Protein SPT2 homolog	SPTY2D1	GPGRPVSSPHELR_S7	NWF	39.39	0.00023	93.53%	ADP-Ribosyl-EThcD (SRDEKY) (DEKRSY)	464	476
Q68D10	Protein SPT2 homolog	SPTY2D1	RPVSGLGPPGR_R1	NWF	36.85	0.00069	98.69%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	477	487
Q68D10	Protein SPT2 homolog	SPTY2D1	TVSNSVPGRPVSSLGPGQTVSSSGPTIKPK_S5	NWF	54.9	7.10E-06	45.23%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	505	534
Q01130	Serine/arginine-rich splicing factor 2	SRSF2	SYGRPPPDVEGMTSLK_K16	NWF	28.76	0.0023	61.64%	Acetyl (Protein N-term); ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	2	17
J3KP15	Serine/arginine-rich-splicing factor 2 (Fragment)	SRSF2	SYGRPPPDVEGMTSLK_S1	NWF	40.29	0.00017	82.30%	Acetyl (Protein N-term); ADP-Ribosyl-EThcD (SRDEKY) (DEKRSY)	2	17
Q01130	Serine/arginine-rich splicing factor 2	SRSF2	SYGRPPPDVEGMTSLK_S14	NWF	20.98	0.011	60.44%	Acetyl (Protein N-term); ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	2	17
Q92804	TATA-binding protein-associated factor 2N	TAF15	SGGGYGGDR_S1	NWF	25.25	0.0078	100%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	423	431
Q92804	TATA-binding protein-associated factor 2N	TAF15	SGGYGGDR_S1	NWF	33.06	0.018	99.50%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	546	553
Q92804	TATA-binding protein-associated factor 2N	TAF15	SSGGGYSGDR_S1	NWF	35.78	0.00044	87.25%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	432	441
Q92804	TATA-binding protein-associated factor 2N	TAF15	SSGGGYSGDR_S2	NWF	22.35	0.008	19.32%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	432	441
P11387	DNA topoisomerase 1	TOP1	SGDHLHNDSQIEADFR_S1	NWF	39.46	2.00E-04	78.08%	Acetyl (Protein N-term); ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	2	17
P11387	DNA topoisomerase 1	TOP1	SMMNLQTK_S1	NWF	21.73	0.0096	100%	2 Oxidation (M); ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	643	650
P11388	DNA topoisomerase 2-alpha	TOP2A	DPALNSGVSQKPDPAK_D1	NWF	60.78	1.40E-05	99.84%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	1444	1459
P11388	DNA topoisomerase 2-alpha	TOP2A	DPALNSGVSQKPDPAK_S6	NWF	31.91	0.001	95.83%	ADP-Ribosyl-EThcD (SRDEKY) (DEKRSY)	1444	1459
P11388	DNA topoisomerase 2-alpha	TOP2A	RDPALNSGVSQKPDPAK_D14	NWF	56.27	7.30E-06	56.74%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	1443	1459
P11388	DNA topoisomerase 2-alpha	TOP2A	RDPALNSGVSQKPDPAK_K17	NWF	43.29	0.00019	31.50%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	1443	1459
P11388	DNA topoisomerase 2-alpha	TOP2A	RDPALNSGVSQKPDPAK_S7	NWF	70.66	2.70E-07	99.90%	ADP-Ribosyl-EThcD (SRDEKY) (DEKRSY)	1443	1459
P11388	DNA topoisomerase 2-alpha	TOP2A	SKGESDDFHMDFDSAVAPR_K2	NWF	57.98	3.70E-06	48.16%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	1491	1509
Q14669	E3 ubiquitin-protein ligase TRIP12	TRIP12	SGSGSESTGAEER_S1	NWF	44.78	6.30E-05	85.10%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	159	171
V9GYR5	Upstream stimulatory factor 2	USF2	SGGADSGGHHQRPAGGVR_S1	NWF	65.96	8.00E-07	99.80%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	70	87
Q96S55	ATPase WRNIP1	WRNIP1	SGQSYSPSR_S1	NWF	28.89	0.002	98.59%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	465	473
P25490	Transcriptional repressor protein YY1	YY1	KSYLSGGAGAAGGGGADPGNK_S5	NWF	68.28	4.00E-07	99.27%	ADP-Ribosyl-EThcD (SRDEKY) (DEKRSY)	183	203
P25490	Transcriptional repressor protein YY1	YY1	KSYLSGGAGAAGGGGADPGNKK_K1	NWF	67.49	5.80E-07	84.40%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	183	204
P25490	Transcriptional repressor protein YY1	YY1	KSYLSGGAGAAGGGGADPGNKK_K21	NWF	32.88	0.0013	49.00%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	183	204
P25490	Transcriptional repressor protein YY1	YY1	SYLSGGAGAAGGGGADPGNK_S4	NWF	62.16	1.50E-06	88.18%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	184	203
P25490	Transcriptional repressor protein YY1	YY1	SYLSGGAGAAGGGGADPGNKK_S4	NWF	37.12	0.00061	48.08%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	184	204
P25490	Transcriptional repressor protein YY1	YY1	SYLSGGAGAAGGGGADPGNKK_Y2	NWF	81.24	7.20E-08	49.58%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	184	204
Q8IXZ2	Zinc finger CCCH domain-containing protein 3	ZC3H3	SGTSPAATAK_S1	NWF	22.05	0.0085	93.00%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	462	471
Q8IXZ2	Zinc finger CCCH domain-containing protein 3	ZC3H3	SVGSVGDSPREPR_S1	NWF	26.07	0.0075	91.56%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	204	216
Q9NR11	Zinc finger protein 302	ZNF302	SGAAFNQSK_S1	NWF	31.61	0.0083	93.98%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	258	266
Q96KM6	Zinc finger protein 512B	ZNF512B	SVPVTKPVPVTKPITVTK_S1	NWF	43.75	7.90E-05	98.45%	ADP-Ribosyl-HCD_249_347_583 (DEKRSY)	263	280
Q14966	Zinc finger protein 638	ZNF638	SGHGTEFNK_S1	NWF	36.75	0.00036	100%	ADP-Ribosyl-EThcD (SRDEKY) (DEKRSY)	585	593

Table 3: detailed information on peptides, modification sites and proteins identified in the WBL of control pigs.

UniProt ID	prot_desc	gene_name	plasma_prot	PEP_ADPr_site	pep_score	pep_expect	pep_var_mod_conf	pep_var_mod	pep_start	pep_end
I3LEN2	Uncharacterized protein	ADCYAP1R1	no	KLHCTRNFIHMNLFVSFMLR_S11	18.45	0.026	81.92%	Oxidation (M); ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	173	192
A0A287BRD8	BCL2 associated athanogene 5	BAG5	no	TELQGLIGQLDEVSLEK_S14	16.41	0.036	85.97%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	327	343
F1S8V8	Dynamin binding protein	DNMBP	no	GDEDSLMEK_S5	16.19	0.04	24.69%	Oxidation (M); ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	986	994
F1SHL4	Uncharacterized protein	F1SHL4	no	AKVMKNDPVKKIFVGPR_K4	15.81	0.033	37.24%	Oxidation (M); ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	140	156
A0A286ZZN9	Uncharacterized protein	GFPT2	no	REIIHGLK_K8	17.13	0.029	49.15%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	505	512
P01965	Hemoglobin subunit alpha	HBA	no	AVGHLDDLPGALSALSDLHAHK_D17	27.2	0.0034	20.49%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	69	90
P01965	Hemoglobin subunit alpha	HBA	no	AVGHLDDLPGALSALSDLHAHK_D6	99.67	4.50E-10	90.90%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	69	90
P01965	Hemoglobin subunit alpha	HBA	no	AVGHLDDLPGALSALSDLHAHK_D7	80.32	4.10E-08	93.47%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	69	90
P01965	Hemoglobin subunit alpha	HBA	no	AVGHLDDLPGALSALSDLHAHK_H21	38.44	0.00025	80.41%	ADP-Ribosyl-EThcD (DEHKRSY) (DEHKRSY)	69	90
P01965	Hemoglobin subunit alpha	HBA	no	AVGHLDDLPGALSALSDLHAHK_H4	95.29	1.30E-09	98.90%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	69	90
P01965	Hemoglobin subunit alpha	HBA	no	AVGHLDDLPGALSALSDLHAHK_S13	28.32	0.0068	46.51%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	69	90
P01965	Hemoglobin subunit alpha	HBA	no	AVGHLDDLPGALSALSDLHAHKLR_D6	121.08	4.40E-12	91.30%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	69	92
P01965	Hemoglobin subunit alpha	HBA	no	AVGHLDDLPGALSALSDLHAHKLR_D7	49.12	2.50E-05	71.72%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	69	92
P01965	Hemoglobin subunit alpha	HBA	no	AVGHLDDLPGALSALSDLHAHKLR_H4	89.13	4.40E-09	98.07%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	69	92
P01965	Hemoglobin subunit alpha	HBA	no	FLANVSTVLTSK_K12	17.26	0.024	57.06%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	128	139
P01965	Hemoglobin subunit alpha	HBA	no	FLANVSTVLTSK_S11	39.44	2.00E-04	93.33%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	128	139
P01965	Hemoglobin subunit alpha	HBA	no	FLANVSTVLTSK_S6	17.37	0.023	100%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	128	139
P01965	Hemoglobin subunit alpha	HBA	no	LLSHCLLVTLAAHHPDDFNPSVHASLDK_H13	46.71	4.20E-05	72.11%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	100	127
P01965	Hemoglobin subunit alpha	HBA	no	LLSHCLLVTLAAHHPDDFNPSVHASLDK_H4	23.28	0.0066	28.00%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	100	127
P01965	Hemoglobin subunit alpha	HBA	no	LLSHCLLVTLAAHHPDDFNPSVHASLDK_S3	86.26	8.20E-09	86.56%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	100	127
P01965	Hemoglobin subunit alpha	HBA	no	MFLGFPTTKTYFPHFNLSHGSDQVK_Y11	45.52	6.50E-05	49.75%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	32	56
P01965	Hemoglobin subunit alpha	HBA	no	TYFPHFNLSHGSDQVK_H10	60.5	2.20E-06	92.07%	ADP-Ribosyl-EThcD (DEHKRSY) (DEHKRSY)	41	56
P01965	Hemoglobin subunit alpha	HBA	no	TYFPHFNLSHGSDQVK_H5	74.06	1.10E-07	99.82%	ADP-Ribosyl-EThcD (DEHKRSY) (DEHKRSY)	41	56
P01965	Hemoglobin subunit alpha	HBA	no	TYFPHFNLSHGSDQVK_S12	49.84	2.10E-05	50.52%	ADP-Ribosyl-EThcD (DEHKRSY) (DEHKRSY)	41	56
P01965	Hemoglobin subunit alpha	HBA	no	TYFPHFNLSHGSDQVK_Y2	67.1	7.00E-07	99.87%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	41	56
P01965	Hemoglobin subunit alpha	HBA	no	VGGQAGAHGAEALER_E14	25.02	0.0095	90.23%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	17	31
P01965	Hemoglobin subunit alpha	HBA	no	VGGQAGAHGAEALER_H8	24.67	0.0049	94.25%	ADP-Ribosyl-EThcD (DEHKRSY) (DEHKRSY)	17	31
P04246	Hemoglobin subunit theta	HBE1	no	LSELHCDKLHVDPENFR_E3	35.86	0.00043	41.06%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	88	104
P04246	Hemoglobin subunit theta	HBE1	no	LSELHCDKLHVDPENFR_H5	36.93	0.00034	82.68%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	88	104
F1REX8	Uncharacterized protein	HIP1R	no	NSIKNVPAR_K4	22.54	0.03	100%	Acetyl (Protein N-term); ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	2	10
A0A287BC41	Uncharacterized protein	LMTK2	no	LKEPDVEGKYLGK_K2	16.08	0.043	84.02%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	1251	1263
I3LCS1	Uncharacterized protein	LOC100624559	no	HLNDLK_K6	16.95	0.044	100%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	59	64
I3LCS1	Uncharacterized protein	LOC100624559	no	HLNDLKK_K7	25.1	0.04	88.94%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	59	65
F1REY1	Lon protease homolog 2 peroxisomal	LONP2	no	TRKHKQDDEKR_K5	18.14	0.039	82.14%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	231	241
A0A286ZMQ5	Uncharacterized protein	MAGEB5	no	DLVEFLWGPK_E4	17.05	0.026	85.08%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	173	182
F1RZG8	Uncharacterized protein	MNS1	no	MKTTQRYIEEFKK_R6	18.78	0.021	73.72%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	238	250
A0A287BGX8	Myin binding protein C slow type	MYBPC1	no	MDLASKAGKHLQLK_K1	15.12	0.043	81.51%	Oxidation (M); ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	1	14
A0A287B1L5	Uncharacterized protein	OGFR	no	FQNLNWHSHNNLR_H7	24.04	0.039	80.71%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	179	191
A0A287B1L5	Uncharacterized protein	OGFR	no	FQNLNWHSHNNLR_H9	28.87	0.0021	57.70%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	179	191
A0A287B1L5	Uncharacterized protein	OGFR	no	FQNLNWHSHNNLR_R13	37.93	0.00064	56.27%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	179	191
A0A287B1L5	Uncharacterized protein	OGFR	no	FQNLNWHSHNNLR_S8	23.55	0.0074	41.95%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	179	191
A0A287B1L5	Uncharacterized protein	OGFR	no	RFQNLNWHSHNNLR_H10	38.26	0.00026	78.89%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	178	191
A0A287B1L5	Uncharacterized protein	OGFR	no	RFQNLNWHSHNNLR_H8	18.8	0.022	57.89%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	178	191
A0A287B1L5	Uncharacterized protein	OGFR	no	RFQNLNWHSHNNLR_R1	75.87	1.80E-07	99.99%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	178	191
A0A287B1L5	Uncharacterized protein	OGFR	no	RFQNLNWHSHNNLR_R14	23.61	0.0073	47.84%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	178	191
I3LTG9	Uncharacterized protein	RAD51D	no	ILQLLQARTSDEEEQAGALQRIQVVR_E14	18.33	0.019	18.58%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	159	184
A0A287A4Z9	Uncharacterized protein	SENP5	no	KYLLTEAR_Y2	19.12	0.042	46.23%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	649	656
F1RU38	Uncharacterized protein	SF3B2	no	QKKRKAQPQDSRGGSK_S15	18.15	0.025	82.35%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	873	888
F1SBK2	Uncharacterized protein	SLX4IP	no	RALQEIVNR_E5	39.14	0.023	97.44%	Acetyl (N-term); ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	164	172
A0A287BB26	Uncharacterized protein	SMC1A	no	ALGAVESIAMKNPK_S7	22.77	0.0099	72.61%	Acetyl (Protein N-term); Oxidation (M); ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	2	15
A0A287BMR4	SRP receptor alpha subunit	SRPRA	no	LIDGIVLTKFDTIDDK_D15	18.8	0.037	45.71%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	581	596
A0A287BLR3	Uncharacterized protein	USP53	no	TGLLFHVDDNSASGK_H6	18.49	0.028	92.65%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	723	737
A0A287B900	Uncharacterized protein	VPS26A	no	YFLNLVLVLVDEEDRR_R14	18.14	0.045	24.15%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	247	260
A0A287ATP7	Uncharacterized protein	YTHDC2	no	GILHPKRSADDR_S8	17.66	0.039	35.43%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	1124	1135
A0A287BKA2	Uncharacterized protein	ZNF317	no	WSILMEDIFGRGPSNGVTVER_S2	21.72	0.032	91.88%	Oxidation (M); ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	58	78
P29700	Alpha-2-HS-glycoprotein (Fragment)	AHSG	yes	HTLNQVDSVK_H1	40.94	0.00014	99.11%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	55	64
P29700	Alpha-2-HS-glycoprotein (Fragment)	AHSG	yes	HTLNQVDSVK_S8	28.7	0.011	58.03%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	55	64
A0A286ZNV5	4-trimethylaminobutyraldehyde dehydrogenase	ALDH9A1	yes	ISFTGSVPTGSK_S2	58.78	6.00E-06	99.96%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	228	239
I3LQH7	Uncharacterized protein	BLVRB	yes	YVAVMPPHIGDQPLTGAYTVTLDGR_Y1	68.42	3.80E-07	99.55%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	146	170
A0A287B6M0	Uncharacterized protein	CA2	yes	IVNNGHSFNVEFDSSQDK_H6	45.57	5.30E-05	88.06%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	59	76
F1SNS3	Uncharacterized protein	CACHD1	yes	GYLVAHPTLIDPK_D11	19.48	0.015	71.38%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	859	871
A0A287AK64	Uncharacterized protein	CFAP54	yes	GLLCVPVDVTDTLR_D11	21.28	0.018	87.92%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	1851	1864
A0A287BBI5	Glyceraldehyde-3-phphate dehydrogenase	GAPDH	yes	VIISAPSADAPMFVMGVNHEK_S4	87.36	1.90E-08	99.91%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	109	129

Table 3: detailed information on peptides, modification sites and proteins identified in the WBL of control pigs (continued).

UniProt ID	prot_desc	gene_name	plasma_prot	PEP_ADPr_site	pep_score	pep_expect	pep_var_mod_conf	pep_var_mod	pep_start	pep_end
P02067	Hemoglobin subunit beta	HBB	yes	FFESFGDLSNADAVMGNPK_E3	109.91	5.00E-11	93.89%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	42	60
P02067	Hemoglobin subunit beta	HBB	yes	FFESFGDLSNADAVMGNPK_S4	67.57	4.60E-07	61.29%	Oxidation (M); ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	42	60
P02067	Hemoglobin subunit beta	HBB	yes	FFESFGDLSNADAVMGNPK_S9	39.86	0.00018	96.64%	ADP-Ribosyl-EThcD (DEHKRSY) (DEHKRSY)	42	60
P02067	Hemoglobin subunit beta	HBB	yes	HLDNLK_H1	33.38	0.037	99.22%	ADP-Ribosyl-EThcD (DEHKRSY) (DEHKRSY)	78	83
P02067	Hemoglobin subunit beta	HBB	yes	HLDNLK_K6	16.95	0.044	100%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	78	83
P02067	Hemoglobin subunit beta	HBB	yes	HLDNLKGTFAK_D3	22.83	0.0093	48.17%	ADP-Ribosyl-EThcD (DEHKRSY) (DEHKRSY)	78	88
P02067	Hemoglobin subunit beta	HBB	yes	HLDNLKGTFAK_H1	39.79	0.00019	98.81%	ADP-Ribosyl-EThcD (DEHKRSY) (DEHKRSY)	78	88
P02067	Hemoglobin subunit beta	HBB	yes	HLDNLKGTFAK_K11	28	0.0024	99.11%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	78	88
P02067	Hemoglobin subunit beta	HBB	yes	KVLQSFSDGLK_K1	64.62	1.00E-05	100.00%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	67	77
P02067	Hemoglobin subunit beta	HBB	yes	KVLQSFSDGLKHLDNLK_K1	91.92	1.30E-08	99.90%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	67	83
F1RII7	Hemoglobin subunit beta	HBB	yes	LGHDFNPDVQAAFQK_D4	78.71	1.50E-06	99.20%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	119	133
F1RII7	Hemoglobin subunit beta	HBB	yes	LGHDFNPDVQAAFQK_H3	63.05	6.10E-05	94.62%	ADP-Ribosyl-EThcD (DEHKRSY) (DEHKRSY)	119	133
F1RII7	Hemoglobin subunit beta	HBB	yes	LGHDFNPDVQAAFQK_K15	68.19	4.60E-06	99.80%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	119	133
P02067	Hemoglobin subunit beta	HBB	yes	LSELHCDQLHVDPENFR_D7	19.67	0.029	34.48%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	89	105
P02067	Hemoglobin subunit beta	HBB	yes	LSELHCDQLHVDPENFR_E14	27.01	0.0029	63.89%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	89	105
P02067	Hemoglobin subunit beta	HBB	yes	LSELHCDQLHVDPENFR_E3	80.34	2.90E-08	91.93%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	89	105
P02067	Hemoglobin subunit beta	HBB	yes	LSELHCDQLHVDPENFR_H10	62.33	1.40E-06	99.11%	ADP-Ribosyl-EThcD (DEHKRSY) (DEHKRSY)	89	105
P02067	Hemoglobin subunit beta	HBB	yes	LSELHCDQLHVDPENFR_H5	75.43	2.00E-07	91.99%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	89	105
P02067	Hemoglobin subunit beta	HBB	yes	LSELHCDQLHVDPENFR_S2	90.98	1.70E-08	94.69%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	89	105
F1RII7	Hemoglobin subunit beta	HBB	yes	RLGHDFNPDVQAAFQK_D5	41	0.0021	91.54%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	118	133
F1RII7	Hemoglobin subunit beta	HBB	yes	RLGHDFNPDVQAAFQK_D9	27.67	0.02	55.04%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	118	133
F1RII7	Hemoglobin subunit beta	HBB	yes	RLGHDFNPDVQAAFQK_H4	53.58	0.00023	89.82%	ADP-Ribosyl-EThcD (DEHKRSY) (DEHKRSY)	118	133
F1RII7	Hemoglobin subunit beta	HBB	yes	RLGHDFNPDVQAAFQK_K16	53.34	1.00E-05	99.96%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	118	133
F1RII7	Hemoglobin subunit beta	HBB	yes	RLGHDFNPDVQAAFQK_R1	43.43	0.00047	91.85%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	118	133
P02067	Hemoglobin subunit beta	HBB	yes	VHLSAEEK_E6	15.32	0.042	40.42%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	2	9
P02067	Hemoglobin subunit beta	HBB	yes	VHLSAEEK_E7	22.53	0.025	62.78%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	2	9
P02067	Hemoglobin subunit beta	HBB	yes	VHLSAEEK_H2	26.88	0.003	100%	ADP-Ribosyl-EThcD (DEHKRSY) (DEHKRSY)	2	9
P02067	Hemoglobin subunit beta	HBB	yes	VHLSAEEK_K8	25.73	0.014	80.55%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	2	9
P02067	Hemoglobin subunit beta	HBB	yes	VHLSAEEK_S4	23.69	0.006	94.22%	ADP-Ribosyl-EThcD (DEHKRSY) (DEHKRSY)	2	9
P02067	Hemoglobin subunit beta	HBB	yes	VLQSFSDGLK_S4	26.72	0.035	96.26%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	68	77
P02067	Hemoglobin subunit beta	HBB	yes	VLQSFSDGLKHLDNLK_D13	24.22	0.0054	38.29%	ADP-Ribosyl-EThcD (DEHKRSY) (DEHKRSY)	68	83
P02067	Hemoglobin subunit beta	HBB	yes	VLQSFSDGLKHLDNLK_H11	16.03	0.031	64.85%	ADP-Ribosyl-EThcD (DEHKRSY) (DEHKRSY)	68	83
P02067	Hemoglobin subunit beta	HBB	yes	VLQSFSDGLKHLDNLK_K16	26.83	0.003	48.88%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	68	83
P02067	Hemoglobin subunit beta	HBB	yes	VLQSFSDGLKHLDNLK_S4	75.01	9.30E-08	99.31%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	68	83
P02067	Hemoglobin subunit beta	HBB	yes	VLQSFSDGLKHLDNLKGTFAK_S4	85.06	1.10E-08	99.13%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	68	88
P02067	Hemoglobin subunit beta	HBB	yes	VNVDEVGGEALGR_D4	24.04	0.0075	83.22%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	19	31
P02067	Hemoglobin subunit beta	HBB	yes	VVAGVANALAHK_H11	32.92	0.0011	96.09%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	134	145
P02067	Hemoglobin subunit beta	HBB	yes	VVAGVANALAHK_K12	48.12	3.50E-05	89.46%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	134	145
P02067	Hemoglobin subunit beta	HBB	yes	VVAGVANALAHKYH_H11	48.26	2.00E-04	96.60%	ADP-Ribosyl-EThcD (DEHKRSY) (DEHKRSY)	134	147
P02067	Hemoglobin subunit beta	HBB	yes	VVAGVANALAHKYH_H14	40.76	0.00015	98.67%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	134	147
P02067	Hemoglobin subunit beta	HBB	yes	VVAGVANALAHKYH_K12	30.54	0.0014	75.91%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	134	147
P02067	Hemoglobin subunit beta	HBB	yes	VVAGVANALAHKYH_Y13	45.67	5.20E-05	83.11%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	134	147
P11708	Malate dehydrogenase cytoplasmic	MDH1	yes	KLSSAMSAAK_K1	43.14	0.0036	98.55%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	239	248
P80895	Protein-L-isoaspartate(D-aspartate) O-methyltransferase	PCMT1	yes	SGGASHSELIHNLR_H11	18.3	0.019	87.86%	ADP-Ribosyl-EThcD (DEHKRSY) (DEHKRSY)	5	18
P80895	Protein-L-isoaspartate(D-aspartate) O-methyltransferase	PCMT1	yes	SGGASHSELIHNLR_H6	33.83	0.012	31.21%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	5	18
P80895	Protein-L-isoaspartate(D-aspartate) O-methyltransferase	PCMT1	yes	SGGASHSELIHNLR_S1	65.14	4.20E-06	99.62%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	5	18
P80895	Protein-L-isoaspartate(D-aspartate) O-methyltransferase	PCMT1	yes	SGGASHSELIHNLR_S5	38.75	0.01	73.49%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	5	18
P80895	Protein-L-isoaspartate(D-aspartate) O-methyltransferase	PCMT1	yes	SGGASHSELIHNLRK_S1	46.04	4.80E-05	99.83%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	5	19
P80895	Protein-L-isoaspartate(D-aspartate) O-methyltransferase	PCMT1	yes	SGGASHSELIHNLRK_S5	34.13	0.00063	67.73%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	5	19

Table 4: detailed information on peptides, modification sites and proteins identified in the WBL of LPS-treated pigs.

UniProt ID	prot_desc	gene_name	plasma_prot	PEP_ADPr_site	pep_seq	pep_score	pep_expect	pep_var_mod_conf	pep_var_mod	pep_start	pep_end
A0A286ZKI5	Uncharacterized protein	ABCC12	no	TFMRDTIMK_D3	TFMRDTIMK	15.96	0.049	47.20%	Oxidation (M); ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	1240	1248
A0A286ZUT6	Uncharacterized protein	AKAP9	no	NAVLDRMAESQEAELER_E7	NAVLDRMAESQEAELER	15.03	0.043	55.67%	Oxidation (M); 2 ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	588	604
A0A287A3V7	Uncharacterized protein	ARID5B	no	AAHGGHSGGASEGPK_S11	AAHGGHSGGASEGPK	19.54	0.026	41.43%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	1056	1070
V5PZZ6	Arrestin domain-containing 5	ARRDC5	no	AERRSKVDSSELLR_R14	AERRSKVDSSELLR	20.77	0.015	91.48%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	225	238
A0A287ADS8	Uncharacterized protein	BEND5	no	RPEGRKPSEVAHK_S8	RPEGRKPSEVAHK	19.45	0.029	66.49%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	229	241
A0A287AJ04	Uncharacterized protein	BICD1	no	QTAEVALANLK_K11	QTAEVALANLK	17.6	0.022	100%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	699	709
F1S7X1	Uncharacterized protein	F1S7X1	no	SMLEEVIANWDR_E2	SMLEEVIANWDR	21.39	0.021	77.37%	Oxidation (M); ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	606	617
A0A286ZL19	Uncharacterized protein	F1SCQ1	no	SFSRKTHLIRHR_R10	SFSRKTHLIRHR	22.91	0.022	82.78%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	509	520
P01965	Hemoglobin subunit alpha	HBA	no	AVGHLDDLPGALSALSDLHAHK_D6	AVGHLDDLPGALSALSDLHAHK	90.13	4.40E-09	89.28%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	69	90
P01965	Hemoglobin subunit alpha	HBA	no	AVGHLDDLPGALSALSDLHAHK_D7	AVGHLDDLPGALSALSDLHAHK	62.16	3.80E-06	98.70%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	69	90
P01965	Hemoglobin subunit alpha	HBA	no	AVGHLDDLPGALSALSDLHAHK_H21	AVGHLDDLPGALSALSDLHAHK	50.08	2.00E-05	92.42%	ADP-Ribosyl-EThcD (DEHKRSY) (DEHKRSY)	69	90
P01965	Hemoglobin subunit alpha	HBA	no	AVGHLDDLPGALSALSDLHAHK_H4	AVGHLDDLPGALSALSDLHAHK	70.07	3.30E-07	98.09%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	69	90
P01965	Hemoglobin subunit alpha	HBA	no	AVGHLDDLPGALSALSDLHAHK_K22	AVGHLDDLPGALSALSDLHAHK	23.21	0.0067	44.82%	ADP-Ribosyl-EThcD (DEHKRSY) (DEHKRSY)	69	90
P01965	Hemoglobin subunit alpha	HBA	no	AVGHLDDLPGALSALSDLHAHK_S13	AVGHLDDLPGALSALSDLHAHK	61.03	1.90E-06	90.52%	ADP-Ribosyl-EThcD (DEHKRSY) (DEHKRSY)	69	90
P01965	Hemoglobin subunit alpha	HBA	no	AVGHLDDLPGALSALSDLHAHKLR_D6	AVGHLDDLPGALSALSDLHAHKLR	103.83	1.90E-10	92.34%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	69	92
P01965	Hemoglobin subunit alpha	HBA	no	AVGHLDDLPGALSALSDLHAHKLR_D7	AVGHLDDLPGALSALSDLHAHKLR	99.54	5.20E-10	49.85%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	69	92
P01965	Hemoglobin subunit alpha	HBA	no	AVGHLDDLPGALSALSDLHAHKLR_H4	AVGHLDDLPGALSALSDLHAHKLR	93.39	1.80E-09	98.87%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	69	92
P01965	Hemoglobin subunit alpha	HBA	no	FLANVSTVLTSK_S11	FLANVSTVLTSK	36.03	0.00042	96.26%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	128	139
P01965	Hemoglobin subunit alpha	HBA	no	FLANVSTVLTSK_S6	FLANVSTVLTSK	15.7	0.034	100%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	128	139
P01965	Hemoglobin subunit alpha	HBA	no	LLSHCLLVTLAAHHPDDFNPSVHASLDK_H13	LLSHCLLVTLAAHHPDDFNPSVHASLDK	81.93	2.10E-08	64.25%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	100	127
P01965	Hemoglobin subunit alpha	HBA	no	LLSHCLLVTLAAHHPDDFNPSVHASLDK_H14	LLSHCLLVTLAAHHPDDFNPSVHASLDK	22.36	0.016	22.22%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	100	127
P01965	Hemoglobin subunit alpha	HBA	no	LLSHCLLVTLAAHHPDDFNPSVHASLDK_H4	LLSHCLLVTLAAHHPDDFNPSVHASLDK	80.07	3.10E-08	39.46%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	100	127
P01965	Hemoglobin subunit alpha	HBA	no	LLSHCLLVTLAAHHPDDFNPSVHASLDK_S25	LLSHCLLVTLAAHHPDDFNPSVHASLDK	69.5	3.00E-07	80.50%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	100	127
P01965	Hemoglobin subunit alpha	HBA	no	LLSHCLLVTLAAHHPDDFNPSVHASLDK_S3	LLSHCLLVTLAAHHPDDFNPSVHASLDK	79.58	3.50E-08	71.97%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	100	127
P01965	Hemoglobin subunit alpha	HBA	no	LRVDPVNFK_R2	LRVDPVNFK	17.02	0.025	85.77%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	91	99
P01965	Hemoglobin subunit alpha	HBA	no	TYFPHFNLSHGSDQVK_D13	TYFPHFNLSHGSDQVK	24.41	0.0051	29.03%	ADP-Ribosyl-EThcD (DEHKRSY) (DEHKRSY)	41	56
P01965	Hemoglobin subunit alpha	HBA	no	TYFPHFNLSHGSDQVK_H10	TYFPHFNLSHGSDQVK	63.05	1.20E-06	95.27%	ADP-Ribosyl-EThcD (DEHKRSY) (DEHKRSY)	41	56
P01965	Hemoglobin subunit alpha	HBA	no	TYFPHFNLSHGSDQVK_H5	TYFPHFNLSHGSDQVK	38.89	0.00023	98.95%	ADP-Ribosyl-EThcD (DEHKRSY) (DEHKRSY)	41	56
P01965	Hemoglobin subunit alpha	HBA	no	TYFPHFNLSHGSDQVK_S12	TYFPHFNLSHGSDQVK	19.48	0.015	38.74%	ADP-Ribosyl-EThcD (DEHKRSY) (DEHKRSY)	41	56
P01965	Hemoglobin subunit alpha	HBA	no	TYFPHFNLSHGSDQVK_Y2	TYFPHFNLSHGSDQVK	77.1	5.90E-08	99.90%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	41	56
P01965	Hemoglobin subunit alpha	HBA	no	VGGQAGAHGAEALER_E14	VGGQAGAHGAEALER	34.44	0.0048	91.82%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	17	31
P01965	Hemoglobin subunit alpha	HBA	no	VGGQAGAHGAEALER_H8	VGGQAGAHGAEALER	20.32	0.012	92.76%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	17	31
A0A287ANC5	Uncharacterized protein	HEATR5B	no	SALTLVMGALDNPNPILR_S1	SALTLVMGALDNPNPILR	16.47	0.049	100%	Oxidation (M); ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	852	869
A0A287A5I8	Uncharacterized protein	HES2	no	KNLKPLLEK_K1	KNLKPLLEK	20.89	0.011	63.58%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	15	23
A0A286ZIK8	Uncharacterized protein	HSPA4L	no	LKVLATTFDPYLGGR_K2	LKVLATTFDPYLGGR	18.32	0.036	92.06%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	220	234
A0A286ZTE8	Uncharacterized protein	LOC100517659	no	KLRVLSMDKK_K1_R3	KLRVLSMDKK	15.68	0.046	100%	Oxidation (M); 2 ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	183	192
A0A287AWP4	Uncharacterized protein	LOC100624559	no	HLNDLKK_K7	HLNDLKK	25.11	0.024	87.49%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	147	153
A0A286ZN09	Uncharacterized protein	LOC102158372	no	RPPKVNR_K4	RPPKVNR	17.37	0.03	72.63%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	241	247
A0A286ZMQ5	Uncharacterized protein	MAGEB5	no	DLVEFLWGPK_E4	DLVEFLWGPK	17.53	0.048	49.54%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	173	182
A0A286ZMJ9	Alpha-mannidase	MAN2A2	no	SNVLLVPLGDDFR_D11	SNVLLVPLGDDFR	22.1	0.043	48.86%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	416	428
F1RZ25	Uncharacterized protein	MPP1	no	RKTLVLIGASGVGR_S10	RKTLVLIGASGVGR	17.41	0.023	100%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	236	249
A0A287AAY6	Uncharacterized protein	MYBPC1	no	MDLASKAGKHLQLK_K1	MDLASKAGKHLQLK	19.35	0.016	87.49%	Oxidation (M); ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	1	14
A0A287A0Y3	Uncharacterized protein	MYO3B	no	VYKVTNKRDGSLAAVK_Y2	VYKVTNKRDGSLAAVK	20.11	0.033	61.19%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	28	43
F1S9A4	Uncharacterized protein	NUCB2	no	EHVMNEVDTNK_E6	EHVMNEVDTNK	16.81	0.03	74.42%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	350	360
A0A287B051	Uncharacterized protein	ODF2	no	LKASFAPMEDK_D8	LKASFAPMEDK	20.41	0.018	46.68%	Oxidation (M); ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	506	516
A0A286ZQ96	Uncharacterized protein	OGFR	no	FQNLNWHSHNNLR_H7	FQNLNWHSHNNLR	18.15	0.04	87.55%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	186	198
A0A286ZQ96	Uncharacterized protein	OGFR	no	FQNLNWHSHNNLR_H9	FQNLNWHSHNNLR	45.92	4.90E-05	88.51%	ADP-Ribosyl-EThcD (DEHKRSY) (DEHKRSY)	186	198
A0A286ZQ96	Uncharacterized protein	OGFR	no	FQNLNWHSHNNLR_R13	FQNLNWHSHNNLR	24.57	0.005	36.85%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	186	198
A0A286ZQ96	Uncharacterized protein	OGFR	no	FQNLNWHSHNNLR_S8	FQNLNWHSHNNLR	21.61	0.0098	41.26%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	186	198
A0A286ZQ96	Uncharacterized protein	OGFR	no	RFQNLNWHSHNNLR_H10	RFQNLNWHSHNNLR	24.23	0.0053	33.39%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	185	198
A0A286ZQ96	Uncharacterized protein	OGFR	no	RFQNLNWHSHNNLR_H8	RFQNLNWHSHNNLR	16.35	0.033	52.56%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	185	198
A0A286ZQ96	Uncharacterized protein	OGFR	no	RFQNLNWHSHNNLR_R1	RFQNLNWHSHNNLR	75.42	3.10E-07	99.91%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	185	198
I3LRU7	DNA-binding protein SATB	SATB2	no	KEEDPRTASQSLLVNLR_S9	KEEDPRTASQSLLVNLR	20.49	0.035	36.59%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	400	416
F1RU38	Uncharacterized protein	SF3B2	no	QKKRKAQPQDSRGGSK_S15	QKKRKAQPQDSRGGSK	18.51	0.037	82.62%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	873	888
F1RMN6	Sphingomyelin phosphodiesterase	SMPD1	no	LDSFLRVPSLR_S3	LDSFLRVPSLR	40.31	0.011	88.75%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	21	31
A0A287BMR4	SRP receptor alpha subunit	SRPRA	no	LIDGIVLTKFDTIDDK_D15	LIDGIVLTKFDTIDDK	20.3	0.03	46.46%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	581	596
A0A287B900	Uncharacterized protein	VPS26A	no	YFLNLVLVDEEDRR_R13	YFLNLVLVDEEDRR	19.07	0.039	31.13%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	247	260
I3LE67	Zinc finger protein 518B	ZNF518B	no	RESADGGSAPR_D5	RESADGGSAPR	17.55	0.032	46.33%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	860	870
P29700	Alpha-2-HS-glycoprotein (Fragment)	AHSG	yes	HTLNQVDSVK_H1	HTLNQVDSVK	19.43	0.015	100%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	55	64
A0A286ZNV5	4-trimethylaminobutyraldehyde dehydrogenase	ALDH9A1	yes	ISFTGSVPTGSK_S2	ISFTGSVPTGSK	70.53	5.80E-07	99.99%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	228	239
A0A287AI92	Uncharacterized protein	CA1	yes	HDTSLKPISVSYNPATAK_S4	HDTSLKPISVSYNPATAK	51.62	1.40E-05	66.09%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	41	58
A0A287B6M0	Uncharacterized protein	CA2	yes	IVNNGHSFNVEFDSSQDK_H6	IVNNGHSFNVEFDSSQDK	46.22	4.60E-05	64.36%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	59	76
A0A287AK64	Uncharacterized protein	CFAP54	yes	GLLCVPVDVTDTLR_D11	GLLCVPVDVTDTLR	16.83	0.04	85.75%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	1851	1864
P00355	Glyceraldehyde-3-phphate dehydrogenase	GAPDH	yes	VIISAPSADAPMFVMGVNHEK_S4	VIISAPSADAPMFVMGVNHEK	90.59	1.40E-08	99.88%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	117	137

Table 4: detailed information on peptides, modification sites and proteins identified in the WBL of LPS-treated pigs (continued).

UniProt ID	prot_desc	gene_name	plasma_prot	PEP_ADPr_site	pep_seq.1	pep_score	pep_expect	pep_var_mod_conf	pep_var_mod	pep_start	pep_end
P02067	Hemoglobin subunit beta	HBB	yes	FFESFGDLSNADAVMGNPK_D7	FFESFGDLSNADAVMGNPK	59.95	3.30E-06	32.71%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	42	60
P02067	Hemoglobin subunit beta	HBB	yes	FFESFGDLSNADAVMGNPK_E3	FFESFGDLSNADAVMGNPK	67.2	5.00E-07	95.12%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	42	60
P02067	Hemoglobin subunit beta	HBB	yes	FFESFGDLSNADAVMGNPK_S4	FFESFGDLSNADAVMGNPK	48.92	2.60E-05	50.86%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	42	60
P02067	Hemoglobin subunit beta	HBB	yes	FFESFGDLSNADAVMGNPK_S9	FFESFGDLSNADAVMGNPK	15.48	0.035	45.72%	ADP-Ribosyl-EThcD (DEHKRSY) (DEHKRSY)	42	60
P02067	Hemoglobin subunit beta	HBB	yes	HLDNLKGTFAK_D3	HLDNLKGTFAK	21.99	0.0087	49.23%	ADP-Ribosyl-EThcD (DEHKRSY) (DEHKRSY)	78	88
P02067	Hemoglobin subunit beta	HBB	yes	HLDNLKGTFAK_H1	HLDNLKGTFAK	38.58	0.00031	88.05%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	78	88
P02067	Hemoglobin subunit beta	HBB	yes	HLDNLKGTFAK_K11	HLDNLKGTFAK	47.69	1.00E-04	99.88%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	78	88
P02067	Hemoglobin subunit beta	HBB	yes	HLDNLKGTFAK_K6	HLDNLKGTFAK	23.28	0.0066	96.28%	ADP-Ribosyl-EThcD (DEHKRSY) (DEHKRSY)	78	88
P02067	Hemoglobin subunit beta	HBB	yes	KVLQSFSDGLK_K1	KVLQSFSDGLK	74.66	4.70E-06	100.00%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	67	77
P02067	Hemoglobin subunit beta	HBB	yes	KVLQSFSDGLKHLDNLK_K1	KVLQSFSDGLKHLDNLK	82.37	1.60E-07	99.91%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	67	83
F1RII7	Hemoglobin subunit beta	HBB	yes	LGHDFNPDVQAAFQK_D4	LGHDFNPDVQAAFQK	86.43	2.80E-07	99.57%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	119	133
F1RII7	Hemoglobin subunit beta	HBB	yes	LGHDFNPDVQAAFQK_H3	LGHDFNPDVQAAFQK	43.14	0.00027	90.05%	ADP-Ribosyl-EThcD (DEHKRSY) (DEHKRSY)	119	133
F1RII7	Hemoglobin subunit beta	HBB	yes	LGHDFNPDVQAAFQK_K15	LGHDFNPDVQAAFQK	72.69	2.60E-06	99.24%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	119	133
P02067	Hemoglobin subunit beta	HBB	yes	LSELHCDQLHVDPENFR_D7	LSELHCDQLHVDPENFR	25.16	0.041	47.88%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	89	105
P02067	Hemoglobin subunit beta	HBB	yes	LSELHCDQLHVDPENFR_E14	LSELHCDQLHVDPENFR	60.54	2.70E-06	51.25%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	89	105
P02067	Hemoglobin subunit beta	HBB	yes	LSELHCDQLHVDPENFR_E3	LSELHCDQLHVDPENFR	80.93	6.00E-08	84.31%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	89	105
P02067	Hemoglobin subunit beta	HBB	yes	LSELHCDQLHVDPENFR_H10	LSELHCDQLHVDPENFR	50.63	3.00E-05	97.88%	ADP-Ribosyl-EThcD (DEHKRSY) (DEHKRSY)	89	105
P02067	Hemoglobin subunit beta	HBB	yes	LSELHCDQLHVDPENFR_H5	LSELHCDQLHVDPENFR	72.16	6.70E-07	89.40%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	89	105
P02067	Hemoglobin subunit beta	HBB	yes	LSELHCDQLHVDPENFR_S2	LSELHCDQLHVDPENFR	61.58	1.70E-06	84.35%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	89	105
F1RII7	Hemoglobin subunit beta	HBB	yes	RLGHDFNPDVQAAFQK_D5	RLGHDFNPDVQAAFQK	50.68	0.00017	86.98%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	118	133
F1RII7	Hemoglobin subunit beta	HBB	yes	RLGHDFNPDVQAAFQK_D9	RLGHDFNPDVQAAFQK	22.97	0.045	24.25%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	118	133
F1RII7	Hemoglobin subunit beta	HBB	yes	RLGHDFNPDVQAAFQK_H4	RLGHDFNPDVQAAFQK	40.06	0.00018	87.54%	ADP-Ribosyl-EThcD (DEHKRSY) (DEHKRSY)	118	133
F1RII7	Hemoglobin subunit beta	HBB	yes	RLGHDFNPDVQAAFQK_K16	RLGHDFNPDVQAAFQK	15.76	0.033	100%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	118	133
F1RII7	Hemoglobin subunit beta	HBB	yes	RLGHDFNPDVQAAFQK_R1	RLGHDFNPDVQAAFQK	48.47	0.00015	98.75%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	118	133
P02067	Hemoglobin subunit beta	HBB	yes	VHLSAEEK_E6	VHLSAEEK	15.93	0.048	40.75%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	2	9
P02067	Hemoglobin subunit beta	HBB	yes	VHLSAEEK_E7	VHLSAEEK	23.72	0.02	65.64%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	2	9
P02067	Hemoglobin subunit beta	HBB	yes	VHLSAEEK_H2	VHLSAEEK	22.12	0.02	100%	ADP-Ribosyl-EThcD (DEHKRSY) (DEHKRSY)	2	9
P02067	Hemoglobin subunit beta	HBB	yes	VHLSAEEK_K8	VHLSAEEK	26.54	0.037	82.41%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	2	9
P02067	Hemoglobin subunit beta	HBB	yes	VLQSFSDGLK_K10	VLQSFSDGLK	17.13	0.044	39.28%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	68	77
P02067	Hemoglobin subunit beta	HBB	yes	VLQSFSDGLK_S4	VLQSFSDGLK	30.1	0.017	96.08%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	68	77
P02067	Hemoglobin subunit beta	HBB	yes	VLQSFSDGLKHLDNLK_D13	VLQSFSDGLKHLDNLK	23.06	0.0069	45.91%	ADP-Ribosyl-EThcD (DEHKRSY) (DEHKRSY)	68	83
P02067	Hemoglobin subunit beta	HBB	yes	VLQSFSDGLKHLDNLK_H11	VLQSFSDGLKHLDNLK	20.65	0.021	66.36%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	68	83
P02067	Hemoglobin subunit beta	HBB	yes	VLQSFSDGLKHLDNLK_S4	VLQSFSDGLKHLDNLK	76.74	7.40E-08	99.11%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	68	83
P02067	Hemoglobin subunit beta	HBB	yes	VLQSFSDGLKHLDNLKGTFAK_S4	VLQSFSDGLKHLDNLKGTFAK	104.15	1.70E-10	99.19%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	68	88
P02067	Hemoglobin subunit beta	HBB	yes	VNVDEVGGEALGR_D4	VNVDEVGGEALGR	22.23	0.012	81.53%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	19	31
P02067	Hemoglobin subunit beta	HBB	yes	VVAGVANALAHK_H11	VVAGVANALAHK	32.74	0.0018	97.15%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	134	145
P02067	Hemoglobin subunit beta	HBB	yes	VVAGVANALAHK_K12	VVAGVANALAHK	55.4	9.20E-06	90.24%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	134	145
P02067	Hemoglobin subunit beta	HBB	yes	VVAGVANALAHKYH_H11	VVAGVANALAHKYH	63.08	5.90E-05	98.18%	ADP-Ribosyl-EThcD (DEHKRSY) (DEHKRSY)	134	147
P02067	Hemoglobin subunit beta	HBB	yes	VVAGVANALAHKYH_H14	VVAGVANALAHKYH	62.86	1.30E-06	92.35%	ADP-Ribosyl-EThcD (DEHKRSY) (DEHKRSY)	134	147
P02067	Hemoglobin subunit beta	HBB	yes	VVAGVANALAHKYH_K12	VVAGVANALAHKYH	42.86	9.60E-05	80.46%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	134	147
P02067	Hemoglobin subunit beta	HBB	yes	VVAGVANALAHKYH_Y13	VVAGVANALAHKYH	46.79	4.10E-05	86.30%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	134	147
F1RKY6	Uncharacterized protein	LOC100153093	yes	QARELQRQLAEELVNR_E12	QARELQRQLAEELVNR	20.74	0.017	89.04%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	18	33
P11708	Malate dehydrogenase cytoplasmic	MDH1	yes	KLSSAMSAAK_K1	KLSSAMSAAK	43.51	0.00067	98.92%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	239	248
P80895	Protein-L-isoaspartate(D-aspartate) O-methyltransferase	PCMT1	yes	SGGASHSELIHNLR_S1	SGGASHSELIHNLR	57.08	7.70E-06	99.67%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	5	18
P80895	Protein-L-isoaspartate(D-aspartate) O-methyltransferase	PCMT1	yes	SGGASHSELIHNLR_S5	SGGASHSELIHNLR	51.74	0.0011	47.34%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	5	18
P80895	Protein-L-isoaspartate(D-aspartate) O-methyltransferase	PCMT1	yes	SGGASHSELIHNLRK_H11	SGGASHSELIHNLRK	19.73	0.014	50.75%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	5	19
P80895	Protein-L-isoaspartate(D-aspartate) O-methyltransferase	PCMT1	yes	SGGASHSELIHNLRK_S1	SGGASHSELIHNLRK	36.24	4.00E-04	67.98%	ADPr_HCD_249_347_583 (DEHKRSY) (DEHKRSY)	5	19

Table 5: detailed information on the proteins identified in the input plasma proteome.

prot_acc	prot_desc	gene_name	pep_query	pep_start	pep_end	pep_score	pep_expect	group
A0A287A333	Alpha-1B-glycoprotein	A1BG	19	350	354	23.06	0.045	both
F1SLX2	Uncharacterized protein	A2M	1066	1335	1340	37.88	0.016	both
A0A287A6F6	Uncharacterized protein	ABCC4	851	257	262	30.24	0.046	ctrl only
A0A286ZJ87	Uncharacterized protein	ABCC5	14885	22	31	19.81	0.04	LPS only
A0A286ZKN8	Uncharacterized protein	ABCC8	874	15	19	18.94	0.041	both
F1RGB5	Uncharacterized protein	ACACB	32499	924	937	17.88	0.047	ctrl only
A0A287B863	Aggrecan core protein	ACAN	35790	498	511	34.56	0.00057	both
F1RRW4	Angiotensin-converting enzyme	ACE	6143	236	243	22.71	0.02	both
A0A287B1V5	Uncharacterized protein	ACOT11	27550	80	91	19.96	0.05	ctrl only
P81693	Low molecular weight phosphotyrosine protein phosphatase	ACP1	5980	20	28	33.89	0.0056	ctrl only
A0A287AAR4	Actin cytoplasmic 1	ACTB	1643	329	335	26.97	0.018	LPS only
A0A287A4R1	Uncharacterized protein	ACTBL2	1643	330	336	26.97	0.018	both
A0A287A5G1	Actin gamma 1	ACTG1	1643	207	213	26.97	0.018	both
A0A286ZWJ1	Uncharacterized protein	ACTG2	1643	330	336	26.97	0.018	both
A0A287A4Q7	Actinin alpha 4	ACTN4	38307	883	899	17.55	0.023	ctrl only
A0A286ZYY7	Uncharacterized protein	ADAM20	84	81	85	28.79	0.048	both
I3LKV5	Uncharacterized protein	ADAMTS13	29545	400	412	57.66	6.80E-06	both
A0A287B327	Uncharacterized protein	ADAMTS3	8771	653	661	29.79	0.0043	LPS only
I3L5B0	Uncharacterized protein	ADD2	25195	65	76	22.24	0.017	ctrl only
A0A287AQV7	Uncharacterized protein	ADGRV1	14913	5522	5532	16.91	0.026	both
A0A287AHI7	Uncharacterized protein	ADIPOQ	7306	166	174	28.81	0.002	both
A0A287A363	Uncharacterized protein	AFM	1148	501	506	48.8	0.00059	both
Q8MJ76	Alpha-fetoprotein	AFP	3226	366	373	40.2	0.00016	both
F1RT17	N(4)-(Beta-N-acetylglucosaminyl)-L-asparaginase	AGA	38260	115	131	15.82	0.033	both
A0A287ABP5	Uncharacterized protein	AGT	395	253	258	33.99	0.035	both
F1SPS7	Acylamino-acid-releasing enzyme	AHSG	9334	119	126	40.92	0.0028	both
A0A287B4J2	Adenosylhomocysteinase	AHCY	11469	264	275	37.46	0.00062	ctrl only
A0A286ZPY1	Uncharacterized protein	AHNAK	16394	1028	1038	33.19	0.00077	both
P29700	Alpha-2-HS-glycoprotein (Fragment)	AHSG	3137	216	222	45.9	0.002	both
A0A287AK38	Uncharacterized protein	AHSP	25974	72	84	60.59	2.10E-06	ctrl only
A0A286ZQ79	Adenylate kinase isoenzyme 1	AK1	16771	173	183	19.38	0.02	both
A0A287BDC1	Uncharacterized protein	AKIRIN2	21176	76	86	15.25	0.037	LPS only
A0A287A3Y9	Alcohol dehydrogenase [NADP(+)]	AKR1A1	10747	36	45	35.91	0.0061	ctrl only
A0A287BGW4	Delta-aminolevulinic acid dehydratase	ALAD	15540	287	297	45.67	5.20E-05	ctrl only
P08835	Serum albumin	ALB	360	205	209	38.68	0.0047	both
A0A287AEA5	Aldehyde dehydrogenase family 16 member A1	ALDH16A1	32400	309	321	17.87	0.021	ctrl only
A0A286ZNV5	4-trimethylaminobutyraldehyde dehydrogenase	ALDH9A1	11264	317	326	57.72	1.60E-05	both
A0A286ZYX8	Fructose-bisphosphate aldolase	ALDOA	8012	61	69	46.1	0.00013	both
A0A287B8Z2	Fructose-bisphosphate aldolase	ALDOC	52344	182	204	104.31	1.70E-10	both
A0A287AV93	Uncharacterized protein	ALG5	5219	52	59	33.8	0.018	LPS only
A0A286ZSH7	Arachidonate 15-lipoxygenase	ALOX15	40993	571	586	15.84	0.033	ctrl only
Q1KS52	Acid-labile subunit	ALS	7797	270	277	16.87	0.026	both
F1SN71	Protein AMBP	AMBP	7192	158	165	31.95	0.0019	both
F1SL93	Uncharacterized protein	AMOTL2	24180	523	536	19.63	0.014	ctrl only
P00690	Pancreatic alpha-amylase	AMY2	21259	26	35	40.71	0.00017	LPS only
T1UNN8	Angiopoietin like 8	ANGPTL8	36716	93	106	18.33	0.019	both
A0A287A126	Ankyrin 1	ANK1	36	591	595	41.51	0.00055	ctrl only
A0A287AEE1	Uncharacterized protein	ANK3	2463	394	400	30.08	0.016	ctrl only
A0A286ZN01	Uncharacterized protein	ANKRD12	2222	1224	1230	31.78	0.047	both
A0A287ABU8	Uncharacterized protein	ANKS3	20793	490	500	21.33	0.025	both
A0A286ZR09	Uncharacterized protein	ANLN	4478	660	667	31.03	0.016	both
F1SK03	Aminopeptidase	ANPEP	46360	864	877	33.69	0.00069	ctrl only
A0A286ZJV6	Annexin	ANXA2	9694	113	122	40.33	0.00045	ctrl only
A0A287A531	Annexin	ANXA5	10403	277	285	27.97	0.0063	both
F1S1G7	Amine oxidase	AOC2	4609	103	111	58.23	8.20E-05	both
A0A286ZZR5	Uncharacterized protein	APC2	3621	1539	1546	53.24	0.00017	both
O19063	Serum amyloid P-component	APCS	5598	77	84	20.54	0.028	both
A0A286ZI19	Uncharacterized protein	APLP2	13199	467	475	32.42	0.045	LPS only
A0A287A6K7	Uncharacterized protein	APMAP	10754	377	385	31.22	0.0012	both
P18648	Apolipoprotein A-I	APOA1	6047	142	150	62.55	2.60E-05	both
F1S1A9	Uncharacterized protein	APOA2	12390	68	77	38.64	0.00047	both
O46409	Apolipoprotein A-IV	APOA4	897	288	293	40.13	0.0099	both
A0A287AG13	Uncharacterized protein	APOB	357	1694	1699	36.7	0.015	both
D3Y264	Apolipoprotein C-II	APOC2	4604	53	60	38.91	0.0028	both
P27917	Apolipoprotein C-III	APOC3	4822	72	78	19.78	0.039	both
A0A286ZPG0	Uncharacterized protein	APOC4	13469	58	66	39.56	0.0054	both
A0A287BS37	Apolipoprotein D	APOD	1984	38	44	34.67	0.0012	both
P18650	Apolipoprotein E	APOE	368	132	136	29.1	0.047	both
A0A140TAK8	Uncharacterized protein	APOH	1704	238	243	26.58	0.0043	both
A0A287AVQ5	Apolipoprotein M	APOM	1946	172	178	39.61	0.0046	both
Q68RU1	Ovarian and testicular apolipoprotein N	ApoN	889	233	239	32.95	0.05	both
Q03472	Apolipoprotein R	APOR	26938	160	171	30.25	0.0015	both
A0A287AT23	Aquaporin-1	AQP1	52829	246	265	92.5	2.10E-09	ctrl only
A0A286ZTI3	Uncharacterized protein	ARF1	9662	20	30	26.24	0.0073	ctrl only
A0A287BM57	Uncharacterized protein	ARF2	9662	20	30	26.24	0.0073	ctrl only
A0A287A1L1	Uncharacterized protein	ARF4	9662	20	30	26.24	0.0073	ctrl only
B9V4F0	ADP-ribosylation factor 5	ARF5	9662	20	30	26.24	0.0073	ctrl only
A0A287B2D9	Uncharacterized protein	ARHGAP27	10165	2	10	18.53	0.037	both
A0A287ART1	Uncharacterized protein	ARHGAP31	5955	795	802	22.14	0.034	ctrl only
E7EI20	Rho GDP dissociation inhibitor alpha	ARHGDIA	33158	59	74	77.01	6.00E-08	ctrl only
A0A287AFI5	Uncharacterized protein	ARHGEF3	461	362	367	15.56	0.035	ctrl only
I3LG01	Uncharacterized protein	ARHGEF38	47996	617	633	17.38	0.025	LPS only
A0A286ZZJ2	Uncharacterized protein	ARHGEF7	15128	671	680	27.96	0.018	ctrl only
A0A287AS03	Uncharacterized protein	ARID5A	18319	31	41	29.61	0.014	LPS only
A0A287A0M2	Uncharacterized protein	ARSG	13570	343	352	39.48	0.0002	LPS only
F1RYU5	NAD(P)(+)--arginine ADP-ribosyltransferase	ART3	4553	84	91	20.22	0.022	both
A5GFT7	AS complex locus	AS	9431	169	178	26.05	0.018	LPS only
A0A287AIE6	ATPase ASNA1	ASNA1	14185	176	185	34.23	0.0029	LPS only
F1RSA3	Uncharacterized protein	ASTE1	45734	658	675	17.87	0.029	LPS only
D0G0C7	Antioxidant protein 1 homolog (Yeast)	ATOX1	23788	26	38	36.65	0.00096	ctrl only
A0A287AX66	Phospholipid-transporting ATPase	ATP10D	26659	1306	1318	17.49	0.046	both
P11607	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	68144	353	371	17.49	0.028	LPS only
A0A287AGU2	ATP synthase subunit alpha	ATP5F1A	7309	192	201	15.93	0.032	ctrl only
A0A287BET3	Uncharacterized protein	ATP5F1B	33624	137	151	34.07	0.00064	ctrl only
A0A287BCX5	V-type proton ATPase catalytic subunit A	ATP6V1A	37940	366	382	18.89	0.017	ctrl only
F1RGL1	Phospholipid-transporting ATPase	ATP8B2	45942	141	156	16.8	0.027	LPS only
F1SKG2	Uncharacterized protein	ATR	13776	1956	1965	23.55	0.02	both
A0A286ZI01	Uncharacterized protein	ATXN2	35003	751	764	16	0.039	LPS only
A0A286ZLH6	Uncharacterized protein	AVL9	53504	477	494	15.97	0.032	ctrl only
A0A286ZX01	Vasopressin V1a receptor	AVPR1A	29819	21	33	19.75	0.03	ctrl only
A0A286ZVC3	Uncharacterized protein	AZGP1	9965	91	99	49	0.00019	both
A0A287B7B9	Beta-2-microglobulin	B2M	21179	88	99	77.82	5.10E-08	both
A0A287AIG3	Uncharacterized protein	B4GALT1	4400	181	188	18.75	0.017	both
F1RFK7	Uncharacterized protein	BAIAP2L1	39355	177	190	17.44	0.023	LPS only
A0A287BKD3	Uncharacterized protein	BAZ2B	28265	1548	1559	16.4	0.035	LPS only
I3LT30	Bardet-Biedl syndrome 2 protein homolog	BBS2	1555	276	282	40.05	0.0022	LPS only
A0A287AGY0	Uncharacterized protein	BBX	39846	345	358	26.85	0.0054	LPS only
I3LQH7	Uncharacterized protein	BLVRB	3773	6	14	47.89	0.001	both
F1RKG8	Uncharacterized protein	BP1	11576	29	39	73.04	2.00E-07	LPS only

Table 5: detailed information on the proteins identified in the input plasma proteome (continued).

prot_acc	prot_desc	gene_name	pep_query	pep_start	pep_end	pep_score	pep_expect	group
A0A286ZQ31	Phosphoglycerate mutase	BPGM	4016	173	181	32.58	0.0015	ctrl only
F1S505	BPI fold-containing family A member 1	BPIFA1	25052	73	88	15.04	0.039	LPS only
F1S033	Bromodomain containing 3	BRD3	18696	689	701	16.32	0.049	LPS only
A0A287BBE7	Uncharacterized protein	BRD8	5751	1	9	22.3	0.042	ctrl only
A0A287BBB8	Uncharacterized protein	BRPF3	2009	685	692	31.3	0.027	LPS only
A0A287AJV7	Uncharacterized protein	BSDC1	36782	156	170	24.61	0.048	LPS only
A0A287ADJ5	Uncharacterized protein	BTBD3	12587	305	314	32.99	0.012	ctrl only
F1RS82	Biotinidase	BTD	10487	335	344	46.54	0.00015	both
A0A287AB51	Uncharacterized protein	C12H17orf100	395	1	6	33.99	0.035	ctrl only
F1SIC7	Uncharacterized protein	C15orf59	34613	277	290	18.52	0.033	ctrl only
A0A287BKX0	Uncharacterized protein	C1D	7010	129	138	23.19	0.043	both
A0A287B0Z7	Complement C1q subcomponent subunit A	C1QA	37631	159	173	50.43	1.90E-05	both
A0A286ZKA5	Uncharacterized protein	C1QB	174	115	120	26.89	0.04	both
A0A286ZSJ7	Uncharacterized protein	C1QC	6878	201	210	67.02	7.90E-06	both
A0A287BFU6	Uncharacterized protein	C1R	6538	25	33	31.29	0.014	both
A0A286ZMS2	Uncharacterized protein	C1S	2498	444	451	33.07	0.0083	both
F1RQW7	Uncharacterized protein	C2	8641	828	835	22.17	0.044	both
F1SBS4	Complement C3	C3	1434	599	605	30.41	0.047	both
F1RQW2	Uncharacterized protein	C4A	230	1663	1667	36.63	0.015	both
A0A286ZU55	Uncharacterized protein	C4BPA	8879	262	270	29.34	0.0024	both
A0A287AL92	Uncharacterized protein	C4BPB	6181	228	235	49.01	4.10E-05	both
F1S8R6	Uncharacterized protein	C4orf48	15759	78	87	20.86	0.017	both
A0A286ZKB4	Complement C5a anaphylatoxin	C5	1222	1143	1149	32.72	0.041	both
F1SMI8	Uncharacterized protein	C6	1298	405	410	25.55	0.035	both
Q9TUQ3	Complement component C7	C7	399	373	378	22.28	0.025	both
A0A287B5F3	Uncharacterized protein	C7orf57	39200	191	206	15.57	0.037	both
F1S788	Uncharacterized protein	C8A	9401	475	484	34.06	0.00079	ctrl only
A0A287AT36	Uncharacterized protein	C8B	3791	252	259	73.06	1.70E-06	both
A0A287AFQ4	Uncharacterized protein	C8G	10613	162	170	30.93	0.0045	both
A0A287BH90	Uncharacterized protein	C9	1106	329	335	27.68	0.024	both
A0A287AI92	Uncharacterized protein	CA1	27746	101	114	64.38	9.20E-07	both
A0A287B6M0	Uncharacterized protein	CA2	6405	159	167	39.24	0.00036	both
A0A287ARG0	Uncharacterized protein	CABS1	17719	9	19	16.15	0.031	ctrl only
F1SNS3	Uncharacterized protein	CACHD1	1337	334	339	32.36	0.048	LPS only
A0A287BJU2	Uncharacterized protein	CACTIN	4305	157	163	19.08	0.043	both
F1S710	Uncharacterized protein	CACYBP	940	11	16	36.29	0.025	both
A0A0G2KBD0	Calcitonin gene-related peptide type 1 receptor	CALCRL	29959	324	335	17.18	0.046	both
A0A287BCG9	Uncharacterized protein	CALM1	1766	32	38	28.89	0.017	ctrl only
F1RYI3	Uncharacterized protein	CAND1	19847	1027	1039	48.17	0.00013	ctrl only
F1SMC0	Adenylyl cyclase-associated protein	CAP1	42836	255	272	30.67	0.004	ctrl only
P35750	Calpain-1 catalytic subunit	CAPN1	17613	37	46	48.15	4.70E-05	ctrl only
Q9N2I1	Caspase-1	CASP1	11099	1	9	21.49	0.045	ctrl only
O62839	Catalase	CAT	1695	493	499	35.59	0.017	both
A0A286ZUF4	Uncharacterized protein	CB2	22302	435	445	25.51	0.034	LPS only
Q28960	Carbonyl reductase [NADPH] 1	CBR1	35139	160	174	46.94	4.00E-05	ctrl only
A0A287AXW1	Uncharacterized protein	CCDC121	10657	201	209	15.39	0.045	LPS only
F1SP97	Uncharacterized protein	CCDC191	2345	619	625	37.07	0.025	LPS only
A0A286ZPZ0	Uncharacterized protein	CCDC30	12449	553	561	25.74	0.02	ctrl only
F1SGC2	Uncharacterized protein	CCDC39	7090	408	415	23.97	0.04	LPS only
F1RZ80	Uncharacterized protein	CCDC40	56338	489	506	15.72	0.034	ctrl only
F1RUT6	Uncharacterized protein	CCDC87	814	153	159	47.81	0.0014	LPS only
A0A287AMZ2	T-complex protein 1 subunit gamma	CCT3	12802	439	449	34.77	0.00055	ctrl only
A0A287AKF5	Uncharacterized protein	CCT7	22404	289	300	18.79	0.017	ctrl only
I3LCA2	Uncharacterized protein	CCT8	21914	283	297	32.52	0.00089	ctrl only
F1RQH9	Uncharacterized protein	CD109	24233	1131	1143	56.91	1.80E-05	both
A2SW51	Monocyte differentiation antigen CD14	CD14	5631	65	72	40.06	0.0056	both
A0A286ZZK6	Uncharacterized protein	CD180	401	254	258	40.43	0.0031	both
F1SGT4	Uncharacterized protein	CD44	9782	42	50	38.18	0.0013	both
A0A286ZPI8	Uncharacterized protein	CD55	30620	75	88	29.28	0.037	ctrl only
A0A287AE58	Uncharacterized protein	CD5L	4081	512	518	29.55	0.023	both
F1SAT8	Uncharacterized protein	CD93	51580	70	88	28.66	0.0069	cb
A0A287AEC2	Uncharacterized protein	CDH1	25202	309	322	74.33	3.90E-07	both
F1RFU7	Uncharacterized protein	CDH11	24376	430	441	31.1	0.0012	both
A0A286ZU93	Uncharacterized protein	CDH17	15257	157	168	56.61	0.00011	c
Q8WNW5	Cadherin-5	CDH5	10281	270	280	50.55	0.00011	both
A0A286ZX45	Uncharacterized protein	CELSR1	50695	1866	1883	16.5	0.028	both
I3LRD3	Uncharacterized protein	CENPE	4541	1251	1258	40.53	0.0093	both
A0A287BAP4	Uncharacterized protein	CEP112	3375	261	267	18.06	0.049	LPS only
F1SF36	Uncharacterized protein	CEP85L	4841	117	125	24.6	0.033	both
A0A287AK64	Uncharacterized protein	CFAP54	16039	2866	2875	18.9	0.042	LPS only
Q03710	Complement factor B (Fragment)	CFB	65393	52	76	63.18	1.20E-06	both
P51779	Complement factor D	CFD	19448	167	177	42.59	0.0001	both
A0A286ZJK1	Uncharacterized protein	CFH	2357	519	525	16.7	0.032	both
A0A287AQ20	Uncharacterized protein	CFI	2495	446	452	41.56	0.0027	both
P10668	Cofilin-1	CFL1	11859	2	13	43.99	0.00017	both
Q5G6V9	Cofilin-2	CFL2	20366	82	92	40.28	0.00021	both
F1RWV1	Uncharacterized protein	CFP	35474	438	451	15.28	0.037	both
A0A286ZJL1	Uncharacterized protein	CHD3	45246	50	64	19.68	0.014	LPS only
A0A286ZN07	Uncharacterized protein	CHMP4A	1031	61	67	34.61	0.0085	both
F1S6Q3	Uncharacterized protein	CILP2	11890	714	723	36.21	0.0029	LPS only
A0A287A2B5	Uncharacterized protein	CINP	37923	150	162	16.76	0.031	both
I3LPB5	Creatine kinase B-type	CKB	16302	237	247	20.44	0.033	c
Q5XLD3	Creatine kinase M-type	CKM	3928	359	365	24.3	0.031	both
A0A287AAI1	Uncharacterized protein	CLEC11A	13219	195	205	45.1	0.00011	both
F1SRC8	C-type lectin domain family 3 member B	CLEC3B	9515	81	89	33.2	0.0026	both
A0A287B250	Chloride intracellular channel protein	CLIC1	40086	103	120	19.38	0.015	c
A0A287A988	Uncharacterized protein	CLIC3	7453	193	201	24.14	0.047	both
A0A287ADH9	Chloride intracellular channel protein	CLIC4	15012	239	249	22.77	0.024	both
C0MHR2	Clathrin heavy chain	CLTC	43374	228	245	35.04	0.00052	c
K7GND8	Clusterin	CLU	3888	216	223	46.09	0.00043	both
A0A2C9F3A4	UMP-CMP kinase	CMPK1	26574	59	71	18.01	0.04	ctrl only
A0A287BCC0	Uncharacterized protein	CNIH2	45775	2	17	15.59	0.036	ctrl only
A0A287AJ55	Uncharacterized protein	CNKSR2	67924	343	367	15.82	0.046	LPS only
A0A287A9Q5	Uncharacterized protein	CNTNAP2	4820	173	180	36.43	0.032	ctrl only
A0A286ZK31	Uncharacterized protein	COBLL1	3848	1093	1101	26.35	0.048	ctrl only
A0A286ZXJ1	Uncharacterized protein	COG5	6981	106	115	17.94	0.03	ctrl only
A0A287A8R0	Uncharacterized protein	COL10A1	25293	521	533	41.73	0.00012	LPS only
F1RQJ0	Uncharacterized protein	COL12A1	31235	540	553	15.13	0.038	ctrl only
A0A287BGV6	Uncharacterized protein	COL14A1	51692	899	916	65.43	5.20E-06	LPS only
A0A286ZIL9	Uncharacterized protein	COL18A1	16910	1244	1256	20.33	0.047	both
A0A287A1S6	Uncharacterized protein	COL1A1	13610	1239	1248	41.63	0.0081	both
I3L781	Uncharacterized protein	COL1A2	30989	1273	1286	37.73	0.00029	both
A0A286ZWS8	Uncharacterized protein	COL2A1	13425	1444	1452	25.24	0.0043	both
A0A286ZLV2	Uncharacterized protein	COL6A3	25385	444	456	19.82	0.014	both
A0A287ATF0	Uncharacterized protein	COLEC10	12604	207	216	26.31	0.0051	both
A0A287ADL0	Uncharacterized protein	COLEC11	13183	250	259	37.93	0.0016	both
A0A287AXP9	Collagen beta(1-O)galactosyltransferase 1	COLGALT1	3478	55	62	20.5	0.03	both
F1S902	Uncharacterized protein	COMP	20433	485	496	24.11	0.031	both
A0A286ZQ12	Coatomer subunit gamma	COPG2	35106	516	527	21.08	0.024	LPS only

Table 5: detailed information on the proteins identified in the input plasma proteome (continued).

prot_acc	prot_desc	gene_name	pep_query	pep_start	pep_end	pep_score	pep_expect	group
F1SKB1	Uncharacterized protein	CP	401	44	49	34.37	0.05	both
F1RU03	Uncharacterized protein	CPA6	31550	96	109	19.94	0.02	ctrl only
F1RK01	Uncharacterized protein	CPB2	1609	291	297	37.3	0.024	both
A0A287A983	Carboxypeptidase N subunit 1	CPN1	37997	107	121	102.62	3.40E-09	both
I3LF89	Uncharacterized protein	CPN2	628	348	354	38.89	0.013	both
F1SSS0	Carbamoyl-phosphate synthase 1	CPS1	31940	533	547	76.21	7.10E-08	ctrl only
I3LVL5	Uncharacterized protein	CRISP3	25247	62	74	55	1.10E-05	both
A0A287B1U0	Uncharacterized protein	CRLF3	13162	60	69	26.25	0.043	LPS only
A0A287AL32	Uncharacterized protein	CROCC	5373	1498	1504	28.41	0.033	LPS only
A0A286ZT09	Uncharacterized protein	CROT	48445	228	245	15.9	0.032	ctrl only
A0A287AL17	Uncharacterized protein	CRTAC1	35323	156	168	32.79	0.021	LPS only
A0A287BE96	Uncharacterized protein	CRYBG2	36934	434	448	22.49	0.017	LPS only
F1SRD7	Uncharacterized protein	CSDC2	17743	117	126	31.37	0.024	LPS only
F1RL77	Uncharacterized protein	CSF1R	31470	110	124	65.4	2.90E-06	both
Q0Z8R0	Cystatin	CST3	53962	102	119	25.09	0.0044	both
F1RU34	Cystatin	CST6	56813	126	143	15.84	0.048	ctrl only
F1S1L9	Uncharacterized protein	CSTF2	11846	419	428	19.78	0.046	LPS only
F1SC70	Carboxypeptidase	CTSA	55634	421	439	22.65	0.0075	ctrl only
A0A287BF94	Cathepsin B	CTSB	7501	270	277	22.71	0.038	both
A0A286ZX26	Cathepsin D	CTSD	24304	330	343	20.8	0.013	both
A0A286ZNU3	Uncharacterized protein	CTSV	22951	50	61	22.36	0.02	ctrl only
A0A286ZZB0	Uncharacterized protein	CWF19L2	29178	613	624	18.75	0.034	LPS only
A0A286ZRH9	Uncharacterized protein	CXADR	62538	133	150	17.64	0.022	LPS only
A0A287AQ90	Uncharacterized protein	CXorf57	8980	77	84	28.28	0.047	LPS only
P00172	Cytochrome b5	CYB5A	23620	78	89	40.84	0.00017	ctrl only
A0A286ZPR0	Aromatase 3	CYP19A3	33817	178	190	15.67	0.047	both
A0A287BAM0	Dystroglycan	DAG1	32701	80	95	41.73	0.00012	both
A0A287A3D1	Uncharacterized protein	DBF4	1030	474	479	36.35	0.025	both
A0A287BJR8	Acyl-CoA-binding protein	DBI	43182	17	34	28	0.0024	ctrl only
A0A287B1T7	Uncharacterized protein	DDAH1	14276	71	81	51.98	3.20E-05	ctrl only
A0A286ZLI8	Uncharacterized protein	DDX17	15153	390	401	30.11	0.0071	both
A0A287A3P8	Uncharacterized protein	DDX50	17934	559	569	18.17	0.047	ctrl only
A0A286ZPQ4	Uncharacterized protein	DENND4C	18376	300	310	24.37	0.0052	LPS only
A0A286ZR82	Uncharacterized protein	DERA	34695	107	122	70.53	2.40E-07	ctrl only
P02540	Desmin	DES	4488	409	416	27.53	0.023	ctrl only
F1S1B9	Uncharacterized protein	DHRS11	13856	241	251	47.98	0.00067	ctrl only
I3LRU8	Uncharacterized protein	DHX36	3487	209	215	33.4	0.017	ctrl only
A0A287AIF6	Death inducer-obliterator 1	DIDO1	26558	2	14	16.46	0.037	both
A0A286ZRB0	Uncharacterized protein	DIP2C	7082	126	134	24.41	0.016	LPS only
A0A287ALV3	Uncharacterized protein	DLC1	7101	267	274	31.46	0.035	ctrl only
A0A287BRM0	Uncharacterized protein	DLG5	31	961	965	36.62	0.0091	ctrl only
A0A287AF97	Uncharacterized protein	DNAH10	17609	645	654	18.96	0.035	LPS only
A0A287AHL5	Uncharacterized protein	DNAH7	15112	2330	2340	17.18	0.032	LPS only
A0A286ZSC6	Uncharacterized protein	DNAH8	42713	419	432	15.14	0.038	ctrl only
F1RIJ5	Uncharacterized protein	DNAJC11	3699	444	450	33.38	0.046	LPS only
F1SB54	Uncharacterized protein	DNAJC2	36879	521	533	19.14	0.022	ctrl only
F1SU72	Uncharacterized protein	DNAJC9	36248	38	52	17.38	0.045	LPS only
F1SDY3	Deoxyribonuclease-2-alpha	DNASE2	27861	66	80	20.29	0.036	LPS only
F1RGE0	Uncharacterized protein	DND1	8889	226	234	23.23	0.03	ctrl only
A0A286ZL45	Uncharacterized protein	DOCK2	59655	230	249	18.44	0.043	ctrl only
A0A287A8X2	Uncharacterized protein	DOCK4	5857	1712	1719	16.25	0.034	both
A0A2C9F3H7	Dipeptidyl peptidase 4	DPP4	40148	685	699	30.82	0.0013	both
F1SSP9	Uncharacterized protein	DPP6	70203	59	81	22.11	0.019	LPS only
I3LG81	Uncharacterized protein	DPY19L1	13872	196	205	20.56	0.033	LPS only
A0A287AQA5	Uncharacterized protein	DSEL	68208	597	619	15.08	0.038	LPS only
A0A287ATF2	Uncharacterized protein	DSG2	34199	38	51	25.84	0.0038	both
I3LRN0	Uncharacterized protein	DTX3L	35024	284	298	16.43	0.029	ctrl only
F1S252	Uncharacterized protein	DUSP27	22950	844	853	32.24	0.0054	LPS only
A0A287B3I2	Uncharacterized protein	DYTN	5656	96	104	21.48	0.014	LPS only
A0A287BNU9	Uncharacterized protein	E2F3	26600	156	169	25.56	0.012	LPS only
A0A287AU20	Uncharacterized protein	E2F4	53027	1	20	15.6	0.034	ctrl only
F1RYJ9	Uncharacterized protein	E2F7	12273	1	9	17.35	0.025	LPS only
A0A287A262	Uncharacterized protein	EARS2	38	309	313	31.7	0.011	both
A0A287BHL7	Uncharacterized protein	ECM1	6396	507	516	36.77	0.0024	both
A0A286ZUI3	Uncharacterized protein	EEF1A1	4052	402	410	34.44	0.0031	ctrl only
A0A286ZNV2	Uncharacterized protein	EEF1A2	4052	556	564	34.44	0.0031	ctrl only
F1SDP1	EEF1A lysine methyltransferase 2	EEF1AKMT2	16606	2	15	18.23	0.019	LPS only
F1SHD6	Uncharacterized protein	EEF1B2	31780	8	22	62.1	1.90E-06	ctrl only
Q29387	Elongation factor 1-gamma (Fragment)	EEF1G	25160	397	409	46.12	4.70E-05	ctrl only
A0A287A1E0	Uncharacterized protein	EEF2	10462	400	410	40.29	0.00017	ctrl only
A0A287B922	Uncharacterized protein	EHBP1	10866	1	9	18.88	0.042	ctrl only
A0A287B1T2	Uncharacterized protein	EHD3	21721	77	87	27.87	0.025	ctrl only
I3LDA5	Uncharacterized protein	EHD4	21721	80	90	27.87	0.025	ctrl only
I3LUM9	Eukaryotic translation initiation factor 2 subunit 3	EIF2S3	31275	2	17	39.5	0.00075	ctrl only
A0A286ZPS5	Eukaryotic translation initiation factor 5A	EIF5A2	18459	56	67	21.37	0.011	ctrl only
A0A287B6A2	Uncharacterized protein	ELF2	13053	532	542	16.04	0.041	LPS only
A0A286ZKS3	Engulfment and cell motility 2	ELMO2	12012	252	261	15.59	0.039	ctrl only
A0A287AJA7	Elongation of very long chain fatty acids protein 1	ELOVL1	979	258	263	31.44	0.015	ctrl only
A0A287B6S5	Uncharacterized protein	ENO1	1915	222	228	58.76	0.00014	both
A0A287ANH6	Uncharacterized protein	ENO2	23339	16	28	44.5	0.00043	both
Q1KYT0	Beta-enolase	ENO3	29926	240	253	39.47	0.0005	both
A0A286ZKF8	Uncharacterized protein	ENPP2	9561	988	996	16.53	0.029	both
A0A287A0X7	Uncharacterized protein	EPB41	12645	394	403	20.63	0.04	ctrl only
A0A286ZJ88	Uncharacterized protein	EPB41L1	37358	175	189	61.08	3.70E-06	ctrl only
A0A287BJX0	Uncharacterized protein	EPB42	28274	411	423	52.07	5.90E-05	ctrl only
A0A286ZNB6	Uncharacterized protein	EPHA3	10021	280	289	15.42	0.036	ctrl only
I3LPX6	Uncharacterized protein	ERICH6	42164	172	188	16.15	0.031	ctrl only
Q9GJT2	S-formylglutathione hydrolase	ESD	33007	210	224	25.23	0.0043	ctrl only
F1RHL1	ETS variant 3	ETV3	29404	381	393	15.94	0.041	both
A0A287AJ08	Uncharacterized protein	ETV7	20678	193	205	17.79	0.047	LPS only
F1RW07	Uncharacterized protein	EVPL	17745	731	741	22.28	0.022	ctrl only
A0A287AET8	Exocyst complex component	EXOC6	13814	508	517	16.06	0.031	LPS only
A0A287BES5	Uncharacterized protein	EXPH5	54391	1759	1777	15.2	0.037	ctrl only
A0A286ZNT6	Uncharacterized protein	EXTL2	5028	209	215	40.75	0.0035	ctrl only
A0A286ZVZ2	Uncharacterized protein	EXTL3	50	422	426	29.53	0.046	ctrl only
F1RN41	Uncharacterized protein	F10	3530	415	423	17.42	0.03	both
A0A286ZR66	Uncharacterized protein	F11	38328	535	548	32.3	0.00094	ctrl only
O97507	Coagulation factor XII	F12	130	578	582	42.3	0.0023	both
K7GQL2	Coagulation factor XIII A chain	F13A1	934	539	544	19.61	0.014	both
A0A287AFP8	Uncharacterized protein	F13B	15989	300	309	22.83	0.0087	both
F1SIB1	Prothrombin	F2	391	463	468	33.73	0.035	both
Q9GLP1	Coagulation factor V	F5	927	1030	1035	36.8	0.0045	both
P16293	Coagulation factor IX (Fragment)	F9	654	330	335	32.71	0.025	both
A0A2C9F382	Fatty acid-binding protein liver	FABP1	17470	44	54	18.57	0.018	LPS only
A0A286ZKB9	Uncharacterized protein	FAM120B	60367	32	50	16.49	0.037	LPS only
A0A287ACV7	Uncharacterized protein	FAM213A	23792	91	103	23.86	0.0058	ctrl only
A0A287B4D4	Uncharacterized protein	FAM81A	23129	166	177	18.01	0.02	ctrl only
F1RUH9	Uncharacterized protein	FAM8A1	7436	1	9	17.61	0.022	LPS only
A0A287BMP6	Fanconi anemia group C protein homolog	FANCC	3865	47	53	27.42	0.038	LPS only

Table 5: detailed information on the proteins identified in the input plasma proteome (continued).

prot_acc	prot_desc	gene_name	pep_query	pep_start	pep_end	pep_score	pep_expect	group
A0A287A8Z0	Uncharacterized protein	FANCD2OS	32350	165	176	17.71	0.022	ctrl only
I3LC73	Uncharacterized protein	FASN	58541	1704	1722	16.51	0.047	LPS only
A0A286ZYP1	Uncharacterized protein	FBH1	1130	530	535	26.89	0.046	ctrl only
A0A287AL89	Fibulin-1	FBLN1	11985	502	511	31.49	0.0036	both
Q29042	Ficolin-1	FCN1	3728	38	46	60.87	7.30E-06	both
Q29041	Ficolin-2	FCN2	3728	35	43	60.87	7.30E-06	both
I3LCL4	Uncharacterized protein	FER1L5	48869	650	665	19.11	0.048	ctrl only
F1SFI6	Uncharacterized protein	FETUB	7107	59	67	15.52	0.035	both
P14460	Fibrinogen alpha chain (Fragment)	FGA	9779	7	17	31.59	0.029	both
P14477	Fibrinogen beta chain (Fragment)	FGB	28454	1	13	52.93	1.10E-05	both
F1RX35	Uncharacterized protein	FGG	1696	155	161	31.87	0.041	both
A0A287BKJ2	Fibrinogen like 1	FGL1	5810	55	62	46.14	0.001	both
A0A287ACQ1	Uncharacterized protein	FHAD1	17528	397	406	22	0.031	ctrl only
Q2VTP6	Peptidylprolyl isomerase	FKBP1A	28933	59	72	28.01	0.0024	ctrl only
A0A286ZRM3	Uncharacterized protein	FLII	42349	43	57	16.41	0.046	both
A0A286ZPG4	Uncharacterized protein	FLNB	52861	1577	1595	16.46	0.048	LPS only
F1RNA6	Uncharacterized protein	FLOT2	36463	64	78	35.48	0.00047	ctrl only
F1S5Q6	Uncharacterized protein	FLT4	45169	708	723	35.35	0.00048	both
A0A286ZY95	Uncharacterized protein	FN1	1202	1028	1034	43.65	0.0042	both
F1RZZ3	Uncharacterized protein	FN3KRP	49327	83	103	21.73	0.0092	ctrl only
A0A287A309	Formin binding protein 4	FNBP4	2810	197	204	28.63	0.042	LPS only
A0A287BLX2	Uncharacterized protein	FOLR1	6001	216	223	31.48	0.0029	LPS only
A0A287AKZ2	Uncharacterized protein	FRAS1	117	1843	1848	37.36	0.014	LPS only
A0A287A840	Uncharacterized protein	FRMPD2	33551	9	25	37.81	0.0024	both
F1RYK8	Uncharacterized protein	FSIP2	39016	5766	5779	19.19	0.029	both
A0A287AZC9	Uncharacterized protein	FSTL1	43049	235	249	15.69	0.049	both
F1S715	Alpha-L-fucosidase	FUCA2	24389	28	38	31.24	0.0012	both
A0A287BIT3	Alpha-(13)-fucosyltransferase	FUT11	2619	129	136	18.87	0.047	LPS only
A0A286ZS04	Uncharacterized protein	FXR1	22889	475	488	20.1	0.036	ctrl only
A0A286ZLD3	FYN binding protein 1	FYB1	26549	228	242	21.27	0.039	both
A0A286ZY10	Glucose-6-phosphate 1-dehydrogenase	G6PD	13744	499	508	35.42	0.00048	ctrl only
Q9GKX6	Aldose 1-epimerase	GALM	59022	1	21	18.31	0.035	both
A0A286ZQE4	Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	1637	226	232	36.11	0.0021	both
F1RM74	Glyceraldehyde-3-phosphate dehydrogenase	GAPDHS	1637	217	223	36.11	0.0021	ctrl only
A0A287BIU0	Uncharacterized protein	GARNL3	26273	840	853	19.92	0.014	LPS only
I3LN42	GC vitamin D binding protein	GC	1888	364	370	32.72	0.024	LPS only
A0A287ADA9	Uncharacterized protein	GCLC	38132	2	17	81.2	2.40E-08	ctrl only
A0A287AA47	Uncharacterized protein	GCLM	36799	50	64	20.01	0.027	ctrl only
I3L5N5	Uncharacterized protein	GCSAM	11731	2	10	26.32	0.017	LPS only
Q6Q7J2	Rab GDP dissociation inhibitor beta	GDI2	10525	90	98	21.24	0.037	ctrl only
A0A287A1W4	Uncharacterized protein	GFAP	20889	353	363	58.97	1.70E-05	LPS only
I3LDM7	Lactoylglutathione lyase	GLO1	2585	61	67	27.11	0.0082	ctrl only
F1SLB4	Uncharacterized protein	GLS2	80305	415	453	18.03	0.032	LPS only
A0A287AY75	Uncharacterized protein	GOLM1	2460	142	148	34.63	0.043	both
F1RPA7	Glycoprotein 2	GP2	6354	489	497	26.65	0.0039	both
P08059	Glucose-6-phosphate isomerase	GPI	14809	242	252	15.95	0.037	ctrl only
A0A287AHX3	Uncharacterized protein	GPLD1	4571	800	808	74.82	2.50E-06	both
A0A287AG70	Glutathione peroxidase	GPX1	6239	7	17	50.82	0.00037	ctrl only
A0A287AIJ3	Glutathione peroxidase	GPX3	1969	147	152	29.85	0.045	both
O18994	Epididymal secretory glutathione peroxidase	GPX5	17771	184	195	39.21	0.0032	both
A0A287BN68	Uncharacterized protein	GRIN2A	51032	783	802	16.15	0.031	both
A0A287AD92	GrpE protein homolog	GRL1	22071	1	11	15.96	0.045	LPS only
F1SBX5	Uncharacterized protein	GRM3	1637	673	679	25.19	0.026	LPS only
A0A286ZLK2	Uncharacterized protein	GRXCR2	11765	122	130	21.6	0.021	both
P20305	Gelsolin (Fragment)	GSN	336	555	559	29.84	0.043	both
Q9N1F5	Glutathione S-transferase omega-1	GSTO1	1810	123	129	20.39	0.023	ctrl only
A0A287AZ91	Glutathione S-transferase P	GSTP1	36834	84	99	80.81	7.10E-08	ctrl only
A0A286ZI87	Uncharacterized protein	GZMB	7220	202	211	32.44	0.0024	both
A0A287A1S9	Histone H2A	H2AFV	2560	77	83	22.34	0.04	LPS only
A0A286ZYN1	Uncharacterized protein	H6PD	21504	263	273	29.3	0.0018	both
A0A287AZ81	Uncharacterized protein	HABP2	28855	374	386	51.59	0.00016	both
P02067	Hemoglobin subunit beta	HBB	5026	2	9	35.44	0.005	both
P02101	Hemoglobin subunit epsilon	HBE1	17106	32	41	37.63	0.0015	both
K7GNR8	Uncharacterized protein	HBQ1	873	74	79	33.67	0.019	both
F1RGX7	Uncharacterized protein	HBZ	1955	93	99	30.99	0.038	ctrl only
A0A287AU98	Uncharacterized protein	HCFC2	49087	191	207	15.9	0.032	LPS only
A0A286ZSH3	Heme-binding protein 1	HEBP1	44468	126	143	46.27	4.60E-05	ctrl only
F1SHF6	Uncharacterized protein	HECTD1	553	696	701	35.69	0.024	ctrl only
A0A287AHB3	Uncharacterized protein	HECW1	3313	1	8	25.56	0.025	LPS only
A0A287AQV2	Uncharacterized protein	HELZ	5383	937	944	23.18	0.036	ctrl only
A0A286ZKQ1	Beta-hexosaminidase	HEXB	7267	362	370	17.78	0.036	LPS only
A0A286ZMW3	Uncharacterized protein	HGFAC	13774	557	567	42.82	0.00084	both
F1SAH3	Uncharacterized protein	HINFP	7245	355	363	16.16	0.03	ctrl only
F1RKI3	Uncharacterized protein	HINT1	57646	59	82	62.35	1.40E-06	ctrl only
A0A286ZZB7	Histone cluster 1 H1 family member e	HIST1H1E	10446	65	75	66.76	1.80E-06	ctrl only
P06348	Histone H1t	HIST1H1T	10446	68	78	66.76	1.80E-06	ctrl only
F2Z581	Histone cluster 1 H2B family member n	HIST1H2BN	11578	36	44	22.35	0.016	ctrl only
A0A286ZRQ1	Histone H2B	HIST2H2BE	5014	113	121	38.45	0.003	ctrl only
A0A286ZPE3	Uncharacterized protein	HNRNPA1	14808	131	140	51.72	0.00015	ctrl only
A0A286ZI52	Heterogeneous nuclear ribonucleoprotein A2/B1	HNRNPA2B1	9638	55	62	25.47	0.0061	ctrl only
A0A286ZK74	Uncharacterized protein	HNRNPC	19447	18	29	25.92	0.024	both
A0A286ZQN9	Heterogeneous nuclear ribonucleoprotein H1	HNRNPH1	20227	88	98	16.46	0.029	ctrl only
A0A286ZWW2	Uncharacterized protein	HNRNPH2	39959	151	167	58.13	3.50E-06	ctrl only
A0A287A699	Uncharacterized protein	HNRNPK	3099	373	381	24.63	0.02	ctrl only
A0A286ZJR3	Heterogeneous nuclear ribonucleoprotein U	HNRNPU	18039	123	132	40.42	0.00023	ctrl only
A0A2C9F356	Haptoglobin	HP	3112	170	176	39.53	0.011	both
Q45FY6	Hypoxanthine-guanine phosphoribosyltransferase	HPRT1	24440	129	141	51.98	0.00013	ctrl only
P50828	Hemopexin	HPX	925	204	209	31.22	0.0081	both
F1SFI5	Uncharacterized protein	HRG	1540	37	43	40.91	0.0054	both
F1SMZ6	Uncharacterized protein	HS1	3824	9	15	26.25	0.021	LPS only
K7GP28	Uncharacterized protein	HSD17B10	6368	285	293	17.21	0.043	LPS only
O02705	Heat shock protein HSP 90-alpha	HSP90AA1	10479	348	356	15.4	0.036	both
A0A286ZR68	Uncharacterized protein	HSP90AB1	12555	482	491	36.9	0.0013	both
Q29092	Endoplasmin	HSP90B1	17180	103	114	28	0.0024	both
P34930	Heat shock 70 kDa protein 1A	HSPA1A	14013	160	171	38.56	0.0081	LPS only
Q6S4N2	Heat shock 70 kDa protein 1B	HSPA1B	14013	160	171	38.56	0.0081	LPS only
A5A8V7	Heat shock 70 kDa protein 1-like	HSPA1L	14013	162	173	38.56	0.0081	both
F1SA70	Uncharacterized protein	HSPA2	15213	27	37	62.78	3.80E-06	both
A0A287B6J6	Uncharacterized protein	HSPA4	27308	20	33	39.2	0.00027	ctrl only
P34935	Endoplasmic reticulum chaperone BiP (Fragment)	HSPA5	39808	92	108	88.89	4.60E-09	both
Q04967	Heat shock 70 kDa protein 6	HSPA6	15213	28	38	62.78	3.80E-06	ctrl only
A0A286ZPN4	Uncharacterized protein	HSPA8	6108	129	137	18.35	0.019	both
A0A287ADJ2	Stress-70 protein mitochondrial	HSPA9	15751	207	218	33.42	0.0046	LPS only
A0A287ATN8	Uncharacterized protein	HSPD1	3997	293	301	52.92	0.00013	ctrl only
A0A286ZHV7	Uncharacterized protein	HSPG2	42000	4164	4181	35.8	0.00088	both
A0A287AA97	Uncharacterized protein	HUWE1	2526	2115	2121	41.84	0.002	LPS only
Q29545	Inhibitor of carbonic anhydrase	ICA	946	554	560	34.17	0.03	both
F1SHE9	Islet cell autoantigen 1 like	ICA1L	67043	98	118	16.83	0.05	LPS only
A0A287A4X6	Uncharacterized protein	ICOSLG	13155	171	180	32.75	0.006	both

Table 5: detailed information on the proteins identified in the input plasma proteome (continued).

prot_acc	prot_desc	gene_name	pep_query	pep_start	pep_end	pep_score	pep_expect	group
Q6IED5	Interferon alpha inducible protein 6	IFI6	13770	110	120	23.65	0.044	LPS only
K7GNR1	Uncharacterized protein	IFIT2	1715	236	242	31.64	0.031	both
F1RNN4	Uncharacterized protein	IFT81	8840	493	501	19.62	0.029	LPS only
A0A286ZP75	Uncharacterized protein	IGDCC4	24565	75	86	18.83	0.02	both
P24853	Insulin-like growth factor-binding protein 2	IGFBP2	929	178	183	27.71	0.015	both
A0A286ZX24	Immunoglobulin heavy constant delta	IGHD	5162	354	361	34.37	0.0088	both
A0A287B6H1	Uncharacterized protein	IL1RAP	11564	94	103	34.73	0.012	ctrl only
K7GS49	Uncharacterized protein	ILF2	23509	128	141	28.66	0.0021	ctrl only
K7GL83	Uncharacterized protein	ILF3	42238	183	200	45.21	5.80E-05	ctrl only
F1SKI5	Inosine-5˜-monophosphate dehydrogenase	IMPDH2	52369	517	535	20.33	0.012	both
A0A287BPF5	Inhibin beta B chain	INHBB	2153	101	108	29.29	0.046	both
A0A287B0Z8	Uncharacterized protein	INMT	30314	79	91	75.19	1.80E-07	ctrl only
A0A287BAN0	Uncharacterized protein	INO80	41115	496	512	19.34	0.044	ctrl only
F1SFW4	Uncharacterized protein	INTS3	46032	53	67	18.66	0.018	LPS only
A0A286ZVK8	Uncharacterized protein	INTU	220	529	533	36.45	0.039	LPS only
F1RP44	Uncharacterized protein	IPO5	38136	442	457	83.1	1.90E-08	ctrl only
A0A286ZVD9	Uncharacterized protein	IQCA1	32873	279	290	15.73	0.033	both
F1RM42	Uncharacterized protein	IRF2BP1	13236	428	438	15.36	0.048	ctrl only
I3LLF1	Uncharacterized protein	IRS1	23036	627	638	19.64	0.028	LPS only
F1RVE7	Integrin beta	ITGB1	7247	182	190	24.16	0.012	LPS only
K7GP66	Uncharacterized protein	ITGB4	447	758	763	34.1	0.034	LPs only
A0A287AG27	Integrin beta	ITGB8	8073	495	502	31.46	0.0044	both
Q29052	Inter-alpha-trypsin inhibitor heavy chain H1	ITIH1	2138	39	46	29.11	0.0057	both
F1RUM4	Inter-alpha-trypsin inhibitor heavy chain H2	ITIH2	2457	324	330	41.48	0.0079	both
A0A287AP73	Uncharacterized protein	ITIH3	2503	538	544	40.49	0.0052	both
A0A286ZN24	Inter-alpha-trypsin inhibitor heavy chain H4	ITIH4	2134	369	375	31.16	0.036	both
A0A287AT14	Uncharacterized protein	ITIH6	20651	649	659	16.29	0.03	both
A0A287BHZ5	Uncharacterized protein	IWS1	12089	834	843	16.73	0.036	ctrl only
A0A287BAD0	Uncharacterized protein	JAKMIP3	73933	637	658	18.3	0.019	LPS only
A0A287BCR9	Uncharacterized protein	JCAD	1824	1072	1078	15.84	0.049	ctrl only
A0A287B5V2	Uncharacterized protein	JCHAIN	4627	77	84	37.9	0.0013	both
A0A286ZVV5	KAT8 regulatory NSL complex subunit 3	KANSL3	1032	2	7	24.96	0.05	both
I3LEM5	Katanin p60 ATPase-containing subunit A-like 2	KATNAL2	13060	289	300	21.42	0.0098	ctrl only
F1RZ97	Uncharacterized protein	KCNG2	122	292	297	31.57	0.027	both
A0A286ZSP9	Uncharacterized protein	KCNK2	8964	1	10	22.18	0.014	LPS only
A0A286ZIZ1	Uncharacterized protein	KCNT1	36758	927	940	19.18	0.022	ctrl only
I3LMF8	Uncharacterized protein	KCTD1	22843	32	44	24.23	0.016	LPS only
F1RHE6	Potassium channel tetramerization domain containing 12	KCTD12	58799	186	206	52.54	1.20E-05	LPS only
F1S4N3	Lysine (K)-specific demethylase 5B	KDM5B	5048	254	261	23.6	0.044	LPS only
K7GNY3	Uncharacterized protein	KHDRBS3	5020	2	8	16.45	0.038	ctrl only
A0A286ZYF1	Uncharacterized protein	KIAA1109	26031	4273	4284	17.78	0.029	LPS only
A0A287BIC6	Uncharacterized protein	KIAA1522	32114	216	230	15.92	0.032	LPS only
I3LUB8	Kinesin-like protein	KIF5C	7504	596	604	30.26	0.041	ctrl only
A0A287BR34	Kinesin-like protein	KIF9	34399	622	634	18.95	0.02	ctrl only
F1RZN7	Uncharacterized protein	KLKB1	492	36	40	34.15	0.022	both
A0A287B3E8	Uncharacterized protein	KLRB1	49579	15	30	16.59	0.037	LPS only
A0A287A6Z4	Uncharacterized protein	KMT2C	64423	3119	3138	20.61	0.012	both
A0A287AHT8	Uncharacterized protein	KNG1	3075	306	314	40.73	0.0017	both
A0A287AML8	Uncharacterized protein	KNTC1	4745	705	712	24.02	0.039	LPS only
F1RWJ5	Importin subunit beta-1	KPNB1	21193	526	537	66.6	9.90E-07	ctrl only
F1SGG3	Uncharacterized protein	KRT1	3116	67	75	35.92	0.0048	both
I3LDS3	Uncharacterized protein	KRT10	1794	241	247	34.44	0.011	both
A0A286ZP27	Uncharacterized protein	KRT12	1828	135	141	40.58	0.0026	both
F1S0K1	Uncharacterized protein	KRT13	1963	183	189	34.97	0.012	both
A0A287AEL2	Uncharacterized protein	KRT14	1794	238	244	34.44	0.011	both
A0A286ZYN0	Uncharacterized protein	KRT15	1794	192	198	34.44	0.011	both
F1SGG1	Uncharacterized protein	KRT18	1794	152	158	34.44	0.011	both
A0A287BHY5	Uncharacterized protein	KRT2	15619	275	283	43.71	0.00056	both
A0A286ZVQ5	Uncharacterized protein	KRT24	1794	141	147	34.44	0.011	both
F1RXF9	Uncharacterized protein	KRT25	9742	83	91	53.64	6.20E-05	both
F1RXG2	Uncharacterized protein	KRT28	1794	170	176	34.44	0.011	both
I3LDM6	Uncharacterized protein	KRT3	11500	381	389	23.5	0.022	both
A0A286ZPQ6	Uncharacterized protein	KRT4	20991	425	435	58.31	1.80E-05	both
A0A287AZL3	Keratin 5	KRT5	15583	359	368	37.24	0.0033	both
A0A287AG48	Keratin 7	KRT7	4488	398	405	27.53	0.023	ctrl only
A0A286ZIX1	Uncharacterized protein	KRT71	2790	143	149	39.93	0.0052	LPS only
A0A287APM4	Uncharacterized protein	KRT75	2798	150	156	40.16	0.0049	LPS only
A0A286ZJM8	Uncharacterized protein	KRT77	26411	173	184	25.02	0.024	both
A0A287B7K6	Uncharacterized protein	KRT78	4488	445	452	27.53	0.023	both
A0A287A2X0	Uncharacterized protein	KRT79	21282	232	241	38.84	0.0015	both
A0A287A784	Uncharacterized protein	KRT8	4488	402	409	27.53	0.023	both
A0A286ZL11	Uncharacterized protein	KRT80	20199	374	384	24.14	0.028	LPS only
F1SBB3	Uncharacterized protein	LAMA3	19381	2069	2079	16.95	0.041	ctrl only
F1SAE9	Uncharacterized protein	LAMB1	36664	194	208	55.96	5.70E-06	both
A0A287ACS7	Uncharacterized protein	LAMB4	2663	1556	1562	26.14	0.023	ctrl only
A0A287B5Y6	Uncharacterized protein	LBP	12610	469	478	34.27	0.023	both
I3LK29	Phosphatidylcholine-sterol acyltransferase	LCAT	34822	203	214	59.77	2.90E-05	both
F1RRX1	Uncharacterized protein	LCN2	24490	102	113	25.45	0.015	LPS only
A0A287ANV7	Uncharacterized protein	LCP1	5364	245	253	37.12	0.00033	both
A0A286ZNX3	L-lactate dehydrogenase	LDHA	32992	145	158	61.19	1.20E-05	both
A0A287AQS1	L-lactate dehydrogenase B chain	LDHB	5118	163	170	37.11	0.0086	both
A0A286ZRI5	Galectin	LGALS1	30205	101	112	19.21	0.016	both
A0A287A604	Uncharacterized protein	LGALS3BP	3128	346	352	28.03	0.0079	both
A0A287BCT6	Uncharacterized protein	LGMN	31215	301	314	38.43	0.0011	both
A0A287A3S0	Pellino E3 ubiquitin protein ligase family member 2	LI2	30761	90	101	19.46	0.015	LPS only
A0A287B925	Protein lin-7 homolog	LIN7B	2612	16	22	39	0.016	ctrl only
F1RPQ9	Uncharacterized protein	LIPG	50163	130	147	27.64	0.003	LPS only
Q3ZD69	Prelamin-A/C	LMNA	24535	299	311	57.92	2.10E-05	ctrl only
F1SLY4	Uncharacterized protein	LMOD2	8435	343	351	19.87	0.026	ctrl only
F1RKY6	Uncharacterized protein	LOC100153093	4867	148	156	24.34	0.036	LPS only
F1S573	Alpha-amylase	LOC100153854	29168	285	297	31.08	0.0012	both
A0A287AT48	Uncharacterized protein	LOC100153899	1616	152	157	40.4	0.0085	both
F1SR80	Tubulin alpha chain	LOC100158003	23543	81	92	36.11	0.00072	ctrl only
A0A287AMU6	Uncharacterized protein	LOC100158011	9434	93	101	24.72	0.012	ctrl only
A0A287B5W2	Uncharacterized protein	LOC100302368	2406	123	130	49.75	0.00054	both
A0A286ZK96	Histone H2B	LOC100512420	5014	90	98	38.45	0.003	ctrl only
A0A286ZYP5	Uncharacterized protein	LOC100513601	32817	43	56	54.32	1.30E-05	both
F1SPW2	Uncharacterized protein	LOC100513636	10106	270	277	19.96	0.05	LPS only
A0A286ZJ89	Uncharacterized protein	LOC100514282	14863	89	98	25.3	0.011	LPS only
F1RII5	Uncharacterized protein	LOC100515788	7161	134	144	64.9	8.20E-07	both
A0A287A5Z8	Uncharacterized protein	LOC100517145	2241	839	845	28.03	0.029	both
A0A286ZSA5	Uncharacterized protein	LOC100519130	3079	202	209	24.25	0.035	ctrl only
A0A286ZI83	Amine oxidase	LOC100520329	332	349	353	44.22	0.0032	both
A0A287A8N4	C-X-C motif chemokine	LOC100520680	3081	83	90	26.81	0.025	both
F1RL06	Uncharacterized protein	LOC100523213	32916	171	185	105.37	5.00E-10	both
F1SCU8	Uncharacterized protein	LOC100523732	15311	375	383	24.4	0.047	LPS only
F1SQ28	Uncharacterized protein	LOC100523789	63415	213	230	16.87	0.026	ctrl only
A0A287A5S9	Uncharacterized protein	LOC100524773	18724	985	994	22.08	0.032	both
F1RJE4	Uncharacterized protein	LOC100525876	13679	16	25	26.83	0.041	LPS only

Table 5: detailed information on the proteins identified in the input plasma proteome (continued).

prot_acc	prot_desc	gene_name	pep_query	pep_start	pep_end	pep_score	pep_expect	group
A0A286ZIH3	Elongation factor 1-alpha	LOC100620900	4052	424	432	34.44	0.0031	ctrl only
A0A287BS91	Uncharacterized protein	LOC100621288	8169	1	10	22.47	0.027	ctrl only
A0A287ALA1	Uncharacterized protein	LOC100621494	6886	273	282	49.2	0.00097	both
I3LK01	Uncharacterized protein	LOC100621639	1917	131	137	25.73	0.015	LPS only
A0A287A665	Uncharacterized protein	LOC100624628	41467	137	152	25.34	0.0042	ctrl only
A0A287A0J1	Tubulin beta chain	LOC100624785		170	179	42.97	0.0002	ctrl only
K7GLE5	Uncharacterized protein	LOC100626157	4901	127	135	31.52	0.016	ctrl only
A0A286ZPQ9	Uncharacterized protein	LOC100736765	43496	1150	1166	15.93	0.032	LPS only
A0A287AHM5	Uncharacterized protein	LOC100737030	1963	174	180	34.97	0.012	both
A0A287AVL4	Uncharacterized protein	LOC100738425	26279	265	277	15.58	0.049	ctrl only
A0A286ZJQ0	Histone H3	LOC102161782	2221	58	64	40.06	0.0048	ctrl only
A0A287AAR6	Uncharacterized protein	LOC102164346	23123	1041	1051	22.29	0.0081	both
F1RUL9	Uncharacterized protein	LOC102166306	19140	58	68	32.7	0.00086	ctrl only
A0A286ZYZ5	Uncharacterized protein	LOC106504545	1616	68	73	40.4	0.0085	both
A0A286ZTU7	Uncharacterized protein	LOC106504547	931	199	204	30.53	0.043	both
A0A286ZKZ0	Uncharacterized protein	LOC106507258	1917	116	122	25.73	0.015	LPS only
A0A286ZS98	Uncharacterized protein	LOC110255205	126	163	168	37.29	0.014	ctrl only
I3LHA3	Uncharacterized protein	LOC110255463	47824	393	409	15.1	0.043	ctrl only
F1S1G8	Amine oxidase	LOC110256000	332	278	282	44.22	0.0032	both
A0A287AE80	Uncharacterized protein	LOC110256481	13205	99	109	18.49	0.028	ctrl only
A0A286ZVG3	Thymosin beta	LOC110257905	18751	2	12	19.15	0.016	ctrl only
K7GSY4	Uncharacterized protein	LOC110257929	75899	122	145	15.67	0.034	LPS only
I3LHC3	Alpha-amylase	LOC110258046	29464	211	222	25.6	0.0053	both
A0A287BRF1	Uncharacterized protein	LOC110258309	14242	164	173	44.3	0.0012	both
A0A286ZQJ9	Uncharacterized protein	LOC110258310	1753	144	151	31.61	0.012	both
A0A287AAW7	Uncharacterized protein	LOC110258312	2025	179	184	31.57	0.036	both
F1RGX4	Uncharacterized protein	LOC110259958	656	2	8	48.91	0.0015	both
A0A287AVR0	Eukaryotic translation initiation factor 3 subunit C	LOC110260088	23942	878	889	16.83	0.045	ctrl only
A0A287BH91	Uncharacterized protein	LOC110261286	30253	488	500	23.51	0.016	LPS only
A0A287BM11	Uncharacterized protein	LOC396684	1361	225	231	26.7	0.046	both
F1S7K2	Uncharacterized protein	LRG1	5484	320	327	31.64	0.0079	both
K7GS03	Uncharacterized protein	LRP1	19590	771	783	33.83	0.0011	LPS only
A0A287B5N0	Uncharacterized protein	LRRC31	55906	1	16	17.68	0.042	LPS only
F1S3V9	Uncharacterized protein	LRRC41	81521	1	28	21.23	0.015	LPS only
A0A287AG02	Uncharacterized protein	LRRIQ3	18447	511	520	32.44	0.0038	both
F1SQR8	Leukotriene A(4) hydrolase	LTA4H	12918	547	556	20.61	0.017	both
P14632	Lactotransferrin	LTF	10029	538	546	20.29	0.014	both
F1SQ09	Uncharacterized protein	LUM	5250	176	184	45.34	0.0021	both
A0A2C9F343	Lysozyme	LYZ	45190	99	113	78.91	1.90E-07	both
A0A287A837	Uncharacterized protein	LZIC	1206	100	105	34.67	0.018	LPS only
A0A287AEG1	Uncharacterized protein	MACF1	59961	1609	1630	19.05	0.04	LPS only
A0A287AG74	Uncharacterized protein	MAGI2	47067	594	606	19.13	0.025	LPS only
I3L826	alpha-1 2-Mannosidase	MAN1C1	25597	285	297	19.06	0.016	LPS only
A0A287BHP5	Alpha-mannosidase	MAN2B1	35277	822	837	21.51	0.0096	both
F1S106	Uncharacterized protein	MANBA	6719	191	199	15.89	0.048	ctrl only
E0YLM4	Mesencephalic astrocyte-derived neurotrophic factor	MANF	22587	161	171	26.29	0.04	ctrl only
A0A287B4Y9	Uncharacterized protein	MAP2K4	21348	145	155	18.1	0.039	ctrl only
A0A287A5U6	Uncharacterized protein	MAP2K5	608	263	269	30.42	0.022	both
K7GKU8	Uncharacterized protein	MASP2	34674	223	237	39.39	0.0002	both
F1S3V0	Uncharacterized protein	MAST2	55504	1530	1549	15.56	0.04	ctrl only
A0A287AEL3	Uncharacterized protein	MAX	29341	2	13	18.75	0.036	LPS only
Q5U9S1	Mannose-binding protein A	MBL1	6796	106	114	32.12	0.014	both
I3LCF4	Uncharacterized protein	MCM3AP	70459	624	646	19.22	0.03	LPS only
P11708	Malate dehydrogenase cytoplasmic	MDH1	13304	221	230	47.16	0.00037	LPS only
I3LP41	Malate dehydrogenase	MDH2	15408	223	233	22.46	0.03	ctrl only
Q29558	NADP-dependent malic enzyme (Fragment)	ME1	8522	108	116	28.98	0.0045	both
A0A287ABG5	Methionine aminopeptidase	METAP1D	574	206	211	36.38	0.016	ctrl only
A0A286ZL87	Uncharacterized protein	MGA	27842	924	936	17.05	0.032	ctrl only
A0A287A042	Uncharacterized protein	MGAM	4808	1057	1064	52.71	0.0007	both
A0A287A375	Uncharacterized protein	MGAM2	45195	1495	1511	47.71	3.40E-05	both
P80928	Macrophage migration inhibitory factor	MIF	8014	79	87	46.9	0.00087	ctrl only
F1RL22	Matrix metalloproteinase	MMP11	1019	375	379	23.81	0.028	both
F1SV56	Matrix metalloproteinase	MMP13	26969	69	81	18.34	0.019	ctrl only
F1RF11	Uncharacterized protein	MMP2	47848	52	70	34.26	0.00061	both
A0A287B8S7	Uncharacterized protein	MOGS	286	325	329	32.24	0.029	both
A0A286ZSV9	Uncharacterized protein	MORC2	14658	453	463	15.3	0.041	ctrl only
F1RYC6	Uncharacterized protein	MORF4L2	1440	87	92	35.02	0.032	LPS only
A0A287AYL1	Uncharacterized protein	MPP6	7530	480	488	28.89	0.016	ctrl only
F1RWA3	Uncharacterized protein	MRC1	11359	944	952	19.49	0.025	both
A0A287AEW3	Uncharacterized protein	MRPS23	37467	1	15	20.05	0.013	ctrl only
A0A286ZZB9	Uncharacterized protein	MSI1	8204	137	146	25.3	0.035	ctrl only
A0A287AK19	Moesin	MSN	10307	239	247	28.36	0.015	ctrl only
F1SPS6	Uncharacterized protein	MST1	14356	711	720	45.99	4.90E-05	ctrl only
F1SNK3	S-methyl-5~-thioadenosine phosphorylase	MTAP	39322	12	29	55.68	1.10E-05	ctrl only
F1RWE3	Uncharacterized protein	MTPAP	295	164	168	32.36	0.019	ctrl only
K9IVW4	Myotrophin	MTPN	36940	98	114	34.28	0.00061	ctrl only
F1RXM4	MUM1 like 1	MUM1L1	39900	416	429	17.87	0.033	LPS only
A0A287AAA1	Uncharacterized protein	MYCBP2	26056	4012	4024	26.16	0.0072	ctrl only
I3LIE3	Uncharacterized protein	MYH14	35885	1048	1060	17.09	0.045	LPS only
F1SKJ1	Uncharacterized protein	MYH9	32251	328	341	29.48	0.0018	ctrl only
A0A2C9F331	Myosin light polypeptide 6	MYL6	29413	91	103	30.05	0.0031	ctrl only
F1SRM1	Uncharacterized protein	MYO10	24932	1912	1924	20.06	0.018	ctrl only
F1SA47	Uncharacterized protein	MYO1F	8073	762	770	21.39	0.027	ctrl only
A0A286ZQ42	Uncharacterized protein	MYO5C	15756	346	356	15	0.039	LPS only
A0A287AHC3	Uncharacterized protein	MYOF	25254	1704	1714	16.39	0.029	LPS only
A0A287A887	Uncharacterized protein	MYOM2	2014	168	174	29.48	0.033	ctrl only
P02009	Hemoglobin subunit zeta	n/a	1955	93	99	30.99	0.038	LPS only
P62802	Histone H4	n/a	5991	61	68	27.11	0.038	LPS only
P01846	Ig lambda chain C region	n/a	32916	65	79	105.37	5.00E-10	LPS only
Q29126	Protein WAP-3	n/a	24675	52	63	60.95	2.80E-05	ctrl only
P16225	Sodium/potassium ATPase inhibitor SPAI-2	n/a	21375	94	105	25.14	0.026	LPS only
A0A287BE02	Sulfotransferase	n/a	19970	2	12	16.31	0.035	LPS only
P02554	Tubulin beta chain	n/a	11323	242	251	42.97	0.0002	ctrl only
A0A075B7J0	Uncharacterized protein	n/a	3212	64	72	29.01	0.036	both
F1STC5	Uncharacterized protein	n/a	2557	199	206	28.26	0.025	both
A0A287AE24	Uncharacterized protein	n/a	2160	198	205	27.93	0.01	both
I3LJA6	Uncharacterized protein	n/a	8076	66	74	51.76	0.0002	both
F1STC2	Uncharacterized protein	n/a	18719	66	78	75.73	1.40E-07	both
I3L6U3	Uncharacterized protein	n/a	18719	66	78	75.73	1.40E-07	both
F2Z5K9	Uncharacterized protein	n/a	2221	58	64	40.06	0.0048	both
F1S5N8	Uncharacterized protein	n/a	4678	100	107	34.45	0.00059	both
A0A075B7H9	Uncharacterized protein	n/a	3212	86	94	29.01	0.036	both
F1S144	Uncharacterized protein	n/a	12100	82	91	21	0.033	both
A0A286ZJ78	Uncharacterized protein	n/a	8561	71	80	28.95	0.012	both
I3L728	Uncharacterized protein	n/a	11206	31	40	50.57	0.0002	both
A0A286ZKW3	Uncharacterized protein	N4BP2L2	33786	534	546	25.56	0.034	LPS only
K7GNZ3	Uncharacterized protein	NACA	25800	180	192	39.88	0.01	ctrl only
F1ST62	Uncharacterized protein	NACAD	14610	1059	1069	19.04	0.039	LPS only
Q0QVW6	Nicotinamide phosphoribosyltransferase	NAMPT	53513	1	19	16.66	0.027	LPS only

Table 5: detailed information on the proteins identified in the input plasma proteome (continued).

prot_acc	prot_desc	gene_name	pep_query	pep_start	pep_end	pep_score	pep_expect	group
A0A287AFP4	Uncharacterized protein	NAP1L1	20333	54	63	33.08	0.0024	ctrl only
A0A287AEQ6	Uncharacterized protein	NAP1L4	20333	84	93	33.08	0.0024	ctrl only
F1RLB6	Uncharacterized protein	NAPA	23267	7	19	38.84	0.00051	ctrl only
A0A286ZV25	Uncharacterized protein	NAV3	17295	940	951	24.26	0.013	ctrl only
A0A287AU28	Uncharacterized protein	NCAM1	14442	474	485	30.68	0.0038	ctrl only
F1SLS9	Condensin complex subunit 1	NCAPD2	15342	234	243	32.35	0.0046	LPS only
A0A286ZI22	Uncharacterized protein	NCAPG2	31619	160	172	16.52	0.039	LPS only
A0A287B069	Uncharacterized protein	NDFIP1	48735	1	18	17.26	0.024	LPS only
F1SLR1	Uncharacterized protein	NDUFA8	765	97	103	22.45	0.014	LPS only
A0A287BMW6	Uncharacterized protein	NDUFB11	5908	2	11	30.95	0.0067	ctrl only
A0A287AWH6	Uncharacterized protein	NDUFV3	4102	1	8	37.57	0.021	LPS only
A0A286ZRQ6	Uncharacterized protein	NEB	38320	1534	1547	37.24	0.0041	ctrl only
A0A287B1U6	Uncharacterized protein	NELL2	9928	57	65	27.85	0.039	ctrl only
A0A287BP79	Uncharacterized protein	NEU4	24062	84	94	32.21	0.0032	LPS only
A0A287AVR3	Uncharacterized protein	NFKB1	38757	117	130	15.18	0.038	LPS only
A0A286ZL08	Uncharacterized protein	NID1	13207	648	658	22.97	0.022	ctrl only
F1SMG7	Uncharacterized protein	NIM1K	52309	225	244	17.57	0.022	ctrl only
F1SAS0	Uncharacterized protein	NINL	13	505	509	35.46	0.014	LPS only
A0A287AS29	Nucleoside diphosphate kinase	NME1	13368	40	49	64.24	3.80E-06	ctrl only
Q2EN76	Nucleoside diphosphate kinase B	NME2	13185	57	66	24.38	0.048	ctrl only
F1RG17	Nucleoside diphosphate kinase	NME3	20087	24	35	32.15	0.044	ctrl only
F1SUF5	Nucleolar protein 8	NOL8	16917	208	218	16.39	0.038	ctrl only
A0A287A770	Uncharacterized protein	NPTN	405	160	164	17.07	0.047	LPS only
A0A287B2K4	Neuropilin	NRP2	34807	288	303	32.92	0.00082	ctrl only
A0A287AX72	Uncharacterized protein	NSMF	1764	2	8	17.13	0.038	ctrl only
I3L713	NOP2/Sun RNA methyltransferase family member 7	NSUN7	50729	15	36	20.65	0.019	LPS only
A0A286ZWM0	5~-nucleotidase	NT5C3B	6111	121	128	23.94	0.045	LPS only
A0A287AHD5	Uncharacterized protein	NUCB1	20620	150	160	19.39	0.025	LPS only
A0A287ALQ1	Uncharacterized protein	NUP210	29694	129	140	50.29	0.001	LPS only
F1SCL8	Uncharacterized protein	NUTM1	16357	277	285	25.95	0.01	LPS only
I3LNX4	Uncharacterized protein	NXF1	9023	347	355	24.25	0.032	LPS only
Q29599	2~-5~-oligoadenylate synthase 1	OAS1	8681	116	124	27.41	0.0066	both
F1SUE2	Osteomodulin	OMD	14828	167	176	30.91	0.01	both
F1RNC1	Olfactory receptor	OR6K3	9004	132	139	19.24	0.042	LPS only
F1SN68	Alpha-1-acid glycoprotein	ORM1	4457	181	188	30.48	0.0015	both
A0A2C9F365	Osteoclast-stimulating factor 1	OSTF1	2112	117	124	30.03	0.013	both
O19072	Ornithine carbamoyltransferase mitochondrial (Fragment)	OTC	2373	1	8	24.72	0.016	ctrl only
A0A287A1K0	Uncharacterized protein	OXR1	16323	10	19	18.29	0.048	ctrl only
I3L7I0	Uncharacterized protein	P3H1	4469	688	695	22.9	0.037	LPS only
G9F6X8	Protein disulfide-isomerase	P4HB	14345	317	326	27.49	0.0095	ctrl only
A0A287AZY8	Uncharacterized protein	PABPC5	29664	1	14	18.77	0.017	ctrl only
F1SUK2	P21 (RAC1) activated kinase 1	PAK1	45512	2	16	15.3	0.037	LPS only
F1SQW0	Non-specific serine/threonine protein kinase	PAK2	13007	227	235	16.98	0.037	both
A0A286ZVD4	Pantothenate kinase 4	PANK4	30483	142	153	19.54	0.03	LPS only
Q0R678	DJ-1 protein	PARK7	1916	33	41	35.57	0.0044	ctrl only
I3LDH3	Poly [ADP-ribose] polymerase	PARP1	58363	601	618	18.34	0.028	LPS only
I3LDB1	Poly [ADP-ribose] polymerase	PARP4	12269	97	107	17.76	0.032	ctrl only
A0A287A992	Polysaccharide biosynthesis domain containing 1	PBDC1	26802	157	168	21.45	0.031	LPS only
A0A287BHL0	Uncharacterized protein	PCBP2	21308	20	32	20.16	0.013	ctrl only
A0A287AV49	Protein-L-isoaspartate(D-aspartate) O-methyltransferase	PCMT1	26483	63	76	52.12	0.00074	ctrl only
I3LEE6	Uncharacterized protein	PCOLCE	33796	92	107	68.88	5.30E-07	both
A0A286ZVI0	Uncharacterized protein	PCSK9	14862	124	134	35.38	0.00048	both
F1RNW4	Uncharacterized protein	PD	10363	188	196	42.54	0.0028	both
A0A287A5B4	Uncharacterized protein	PDCD6IP	42424	170	187	29.1	0.0019	ctrl only
E1CAJ6	Protein disulfide isomerase P5	pdi-p5	28715	217	231	39.86	0.00029	both
F6QA08	Protein disulfide-isomerase	PDIA3	13025	335	343	19.63	0.014	ctrl only
A0A286ZSB7	Uncharacterized protein	PDS5B	18757	1042	1051	27.14	0.0054	LPS only
I3LRP4	Uncharacterized protein	PDZD2	7253	1611	1619	18.31	0.045	ctrl only
P30034	Platelet factor 4	PF4	22134	66	76	26.11	0.0054	ctrl only
F1RFY1	Profilin	PFN1	3124	109	116	43.71	0.0025	both
I3L660	Profilin	PFN2	58325	71	89	15.02	0.039	ctrl only
A0A287AJQ2	Phosphoglycerate mutase	PGAM1	38	6	10	31.7	0.011	both
F1RIF8	6-phosphogluconate dehydrogenase decarboxylating	PGD	31274	120	136	33.15	0.00078	ctrl only
F1RPH0	Phosphoglycerate kinase	PGK1	14183	221	230	51.18	0.00091	both
Q6RI85	Phosphoglycerate kinase 2	PGK2	33048	157	171	60.58	2.10E-06	ctrl only
A0A286ZI97	Peptidoglycan-recognition protein	PGLYRP1	57752	199	216	35.03	0.00052	both
A0A287BRX5	N-acetylmuramoyl-L-alanine amidase	PGLYRP2	58828	368	392	26.97	0.003	both
I3LQN4	Uncharacterized protein	PHB2	4569	290	298	24.69	0.031	both
A0A286ZKL5	Uncharacterized protein	PHC3	96	848	852	37.14	0.0085	both
F1RQK4	Pleckstrin homology domain interacting protein	PHIP	12441	1761	1769	19.73	0.017	LPS only
A0A287B268	Uncharacterized protein	PHLPP1	41137	562	576	18.55	0.018	LPS only
F1RVS9	Uncharacterized protein	PI16	30421	34	44	43.08	0.00014	both
A0A287A0N2	Polymeric immunoglobulin receptor	PIGR	25329	535	546	69.05	7.50E-07	both
A0A287AST2	Uncharacterized protein	PIP5K1A	31069	2	14	16.01	0.031	ctrl only
F1RRZ1	Uncharacterized protein	PIP5KL1	17107	220	229	15.37	0.04	ctrl only
A0A286ZWV0	Uncharacterized protein	PKHD1	16110	315	326	21.06	0.046	ctrl only
A0A286ZYV7	Pyruvate kinase	PKLR	11725	325	335	21.14	0.026	ctrl only
A0A287ACX9	Pyruvate kinase	PKM	6017	126	135	41.76	0.0074	both
A0A287A0U1	Platelet-activating factor acetylhydrolase	PLA2G7	24752	357	368	54.78	9.70E-06	both
F1SU38	Urokinase-type plasminogen activator	PLAU	12050	261	269	18.62	0.018	both
A0A287ADQ6	Phosphoinositide phospholipase C	PLCH2	132	784	788	41.86	0.0025	ctrl only
A0A287BPI8	Uncharacterized protein	PLEKHG6	18546	593	604	16.03	0.041	ctrl only
P06867	Plasminogen	PLG	1860	720	726	27.53	0.014	both
I3LA84	Uncharacterized protein	PLOD3	6822	414	422	35.14	0.024	LPS only
A0A286ZJH2	Uncharacterized protein	PLS1	8961	266	274	29.72	0.0018	both
F1RWT2	Plastin 3	PLS3	10698	207	215	30.95	0.0055	both
F1SC57	Uncharacterized protein	PLTP	14445	295	304	22.29	0.011	both
A0A287B8U7	Plexin domain containing 2	PLXDC2	20735	278	289	21.22	0.01	ctrl only
F1SLI0	Uncharacterized protein	PLXNB1	86	1610	1614	29.56	0.036	ctrl only
A0A286ZKJ1	Uncharacterized protein	PMAP-23	28899	45	56	27.42	0.0047	LPS only
A0A286ZR10	Uncharacterized protein	PNKD	27157	129	141	15.74	0.041	ctrl only
A0A287A2Y1	Purine nucleoside phosphorylase	PNP	25436	92	102	29.04	0.0027	ctrl only
A0A287BD23	Uncharacterized protein	POFUT2	3044	345	351	28.9	0.015	both
A0A287B813	Uncharacterized protein	POLA2	24819	2	13	15.6	0.034	ctrl only
F1RMB0	Uncharacterized protein	POLR3D	39507	242	256	16.15	0.031	LPS only
F1SRD5	Uncharacterized protein	POMT2	18385	468	479	20.03	0.025	ctrl only
A0A287AWR7	Uncharacterized protein	PON1	2061	139	145	40.91	0.0052	both
A0A286ZN21	Uncharacterized protein	POSTN	3012	682	689	31.8	0.023	both
P43030	Platelet basic protein	PPBP	3081	83	90	26.81	0.025	both
A0A287A0R3	Uncharacterized protein	PPFIA1	13458	716	726	16.86	0.046	ctrl only
P62936	Peptidyl-prolyl cis-trans isomerase A	PPIA	8413	20	28	44.42	0.00032	both
A0A286ZJY9	Peptidyl-prolyl cis-trans isomerase E	PPIE	12980	244	252	30.61	0.015	ctrl only
A0A286ZL42	Serine/threonine-protein phosphatase	PPP1CA	14045	114	122	24.54	0.0053	ctrl only
F1SDW9	Uncharacterized protein	PPP1R16B	6541	17	24	23.11	0.0068	both
F1RX68	Serine/threonine-protein phosphatase	PPP2CB	38298	75	89	30.67	0.0013	ctrl only
A0A287AHX5	Uncharacterized protein	PPP2R3B	22457	36	46	24.75	0.046	ctrl only
A0A287B775	Uncharacterized protein	PRDM15	4226	656	662	16.72	0.04	ctrl only
A0A286ZND5	Uncharacterized protein	PRDX1	3565	146	153	39.78	0.0065	ctrl only
P52552	Peroxiredoxin-2 (Fragment)	PRDX2	1282	54	61	45.07	0.0015	both

Table 5: detailed information on the proteins identified in the input plasma proteome (continued).

prot_acc	prot_desc	gene_name	pep_query	pep_start	pep_end	pep_score	pep_expect	group
F1SQ01	Uncharacterized protein	PRDX4	4169	202	209	40.66	0.00061	ctrl only
Q9TSX9	Peroxiredoxin-6	PRDX6	3796	156	162	36.25	0.0053	ctrl only
A0A286ZUE0	Uncharacterized protein	PREX1	34169	411	422	16.19	0.048	LPS only
A0A286ZSP2	Uncharacterized protein	PREX2	5879	1158	1165	21.1	0.046	ctrl only
I3L5Z3	Uncharacterized protein	PRG4	25553	339	349	44.82	6.30E-05	both
F1SGF0	Prickle planar cell polarity protein 2	PRICKLE2	24573	1	11	18.2	0.02	both
A0A287A287	Protein kinase C	PRKCD	1082	1	6	29.86	0.045	ctrl only
I3LRJ4	Vitamin K-dependent protein C	PROC	6953	278	285	29.64	0.014	both
I3LQA4	Uncharacterized protein	PROCR	7112	108	116	22.28	0.028	LPS only
A0A287A6Q0	Uncharacterized protein	PROS1	875	317	322	33.07	0.019	both
A0A287AP63	Uncharacterized protein	PRPF3	9937	466	475	25.31	0.033	ctrl only
A0A287B1I2	Uncharacterized protein	PRPH	4488	398	405	27.53	0.023	ctrl only
A0A286ZVG0	Saposin-B-Val	PSAP	19917	295	306	35.71	0.0013	LPS only
F2Z5L7	Proteasome subunit alpha type	PSMA1	1927	108	115	42.02	0.0042	both
I3LAB6	Proteasome subunit alpha type	PSMA2	56853	93	113	24.32	0.0052	ctrl only
F1SSL6	Proteasome subunit alpha type	PSMA3	14779	30	41	37.46	0.00099	both
A0A287BIV4	Proteasome subunit alpha type	PSMA4	15143	55	64	38.6	0.00067	both
F2Z5K2	Proteasome subunit alpha type	PSMA5	8696	11	20	21.21	0.022	both
F2Z5N0	Proteasome subunit alpha type	PSMA6	12382	12	21	32.42	0.042	both
A0A287AT18	Proteasome subunit alpha type	PSMA7	2589	228	234	23.75	0.036	both
F1SBA5	Proteasome subunit alpha type	PSMA8	10174	196	206	41.52	0.00039	both
A0A287BPP9	Proteasome subunit beta	PSMB1	29468	147	160	20.87	0.022	ctrl only
A0A286ZN52	Proteasome subunit beta	PSMB3	29766	178	192	68.42	9.50E-07	both
A0A287B088	Proteasome subunit beta	PSMB4	28859	46	60	41.25	0.00024	both
A0A287AGG3	Proteasome subunit beta	PSMB5	24338	179	191	18.62	0.018	ctrl only
F1RFV5	Proteasome subunit beta	PSMB6	10738	212	222	36.36	0.00095	both
A0A287A1Z0	Proteasome subunit beta	PSMB8	19948	80	91	18.84	0.024	both
A0A287B4P8	Uncharacterized protein	PSMC4	2382	115	121	45.96	0.0027	both
F1RPQ3	Proteasome 26S subunit non-ATPase 14	PSMD14	70063	224	246	19.03	0.016	ctrl only
F1SGM1	Proteasome activator complex subunit 1	PSME1	23624	46	58	58.88	1.30E-05	ctrl only
F1S870	Uncharacterized protein	PSMF1	5107	205	213	26.14	0.04	ctrl only
A0A287AAP9	Uncharacterized protein	PSTK	1969	294	300	26.39	0.025	ctrl only
A0A287APX1	Prostaglandin-H2 D-isomerase	PTGDS	20973	187	198	63.85	1.00E-06	both
C3VVV8	Prothymosin alpha	PTMA	26007	2	15	51.98	1.30E-05	ctrl only
A0A286ZTF3	Serine/threonine-protein phosphatase 2A activator	PTPA	12435	77	86	33.34	0.0024	ctrl only
A0A287AUM0	Uncharacterized protein	PTPN13	23563	1432	1443	21.75	0.047	both
A0A287BMT5	Uncharacterized protein	PTPN18	39685	425	440	15.23	0.04	ctrl only
A0A287AR65	Tyrosine-protein phosphatase non-receptor type	PTPN3	22338	356	366	16.68	0.047	ctrl only
A0A286ZIH1	Uncharacterized protein	PTPRF	36403	586	600	18.07	0.02	both
A0A287BL66	Uncharacterized protein	PTPRG	22762	94	106	59.41	2.70E-06	both
A0A287BN06	Uncharacterized protein	PZP	295	901	905	32.36	0.019	both
F1S682	Sulfhydryl oxidase	QSOX1	4566	318	325	37.12	0.0041	both
F1SIU9	Uncharacterized protein	R2	6147	737	744	23.39	0.043	both
A0A287BKW2	Uncharacterized protein	RAB44	44924	130	147	17.8	0.024	ctrl only
F2Z5I8	Uncharacterized protein	RAB8A	20535	134	145	47.66	7.10E-05	ctrl only
F1RJI2	Uncharacterized protein	RABGEF1	33158	116	129	15.76	0.045	ctrl only
A0A287B104	Uncharacterized protein	RACGAP1	4831	424	430	20.24	0.018	LPS only
A0A287ARC6	Uncharacterized protein	RAD23A	57651	178	204	17.07	0.025	ctrl only
F1RFQ7	GTP-binding nuclear protein Ran	RAN	5156	30	37	29.36	0.013	ctrl only
A0A286ZJ82	Uncharacterized protein	RANBP1	2405	138	144	41	0.004	ctrl only
F1SOW0	Uncharacterized protein	RAPGEF1	38823	335	349	19.3	0.023	LPS only
A0A286ZLM3	Uncharacterized protein	RAPGEF2	1334	621	626	34.06	0.016	both
F1S067	Uncharacterized protein	RAPGEF4	63162	476	497	17.56	0.023	ctrl only
A0A286ZY53	Uncharacterized protein	RARRES2	44785	49	67	55.35	6.80E-06	both
A0A287A0N9	Uncharacterized protein	RB1CC1	13041	1314	1322	37.71	0.0092	LPS only
A0A286ZL66	RNA binding protein fox-1 homolog	RBFOX2	45383	221	237	15.2	0.037	ctrl only
F1SIZ8	Uncharacterized protein	RBM15B	34057	80	98	16.43	0.04	LPS only
A0A287A0L7	Uncharacterized protein	RBM28	219	11	16	28.48	0.043	LPS only
A0A286ZQ71	Uncharacterized protein	RBM45	2438	28	34	25.93	0.021	both
F1SC80	Retinol-binding protein	RBP4	7041	174	181	46.73	0.00042	both
A0A287BMD1	Uncharacterized protein	RC3H2	4800	998	1005	35.42	0.037	ctrl only
I3LMU6	Reticulocalbin 3	RCN3	30420	89	102	97.5	1.00E-08	both
F1SA10	Uncharacterized protein	RCOR1	38539	1	15	20.76	0.029	ctrl only
P26044	Radixin	RDX	10307	238	246	28.36	0.015	ctrl only
F1REY7	Uncharacterized protein	RFESD	35523	87	102	34.96	0.00053	ctrl only
A0A287AKP3	Uncharacterized protein	RFX1	2155	550	557	29.69	0.041	LPS only
F1SBD9	RIPOR family member 3	RIPOR3	27564	674	686	23.86	0.034	ctrl only
I3LBP8	GTP-binding protein Rit1	RIT1	7061	187	195	29.01	0.0093	ctrl only
P15468	Ribonuclease 4	RNASE4	35501	70	82	40.31	0.00034	both
A0A287B8W4	Uncharacterized protein	RNF44	2895	341	348	25.51	0.006	ctrl only
A0A287AM26	Uncharacterized protein	RNP	25420	15	28	24.8	0.0047	ctrl only
A0A286ZKM4	Uncharacterized protein	ROBO3	24011	190	200	18.5	0.047	both
F1STC1	Ribose-5-phosphate isomerase	RPIA	35997	133	147	16.38	0.029	ctrl only
Q29205	60S ribosomal protein L11	RPL11	29522	39	52	48.46	0.00012	ctrl only
A0A287B929	60S ribosomal protein L13a	RPL13A	16140	150	160	34.64	0.0016	ctrl only
A0A286ZW72	60S ribosomal protein L14	RPL14	21123	24	35	57.06	4.50E-06	ctrl only
Q95342	60S ribosomal protein L18	RPL18	20732	86	98	56.05	2.80E-05	ctrl only
A0A287A5S4	Ribosomal protein L19	RPL19	43283	22	38	55.19	6.70E-06	ctrl only
A0A287A286	Uncharacterized protein	RPL24	16491	141	153	44.85	0.00088	ctrl only
A0A287AWS4	60S ribosomal protein L27a	RPL27A	10618	58	68	30.14	0.037	ctrl only
A0A287B5V1	60S ribosomal protein L3	RPL3	5767	11	19	29.83	0.024	ctrl only
A0A287AE76	60S ribosomal protein L4	RPL4	16822	223	234	48.51	3.20E-05	ctrl only
A0A287A8T0	Uncharacterized protein	RPL7	12962	169	179	30.62	0.025	ctrl only
A0A286ZQA5	60S ribosomal protein L7a	RPL7A	20731	174	186	66.69	2.10E-06	ctrl only
A0A287BGL3	60S acidic ribosomal protein P0	RPLP0	14782	17	26	55.41	0.00022	ctrl only
Q29315	60S acidic ribosomal protein P2	RPLP2	16317	50	61	47.49	4.50E-05	ctrl only
F1RZ28	Uncharacterized protein	RPS10	25003	140	153	49.62	2.20E-05	ctrl only
K7GKC0	40S ribosomal protein S16	RPS16	13612	5	15	23.28	0.015	ctrl only
P62272	40S ribosomal protein S18	RPS18	4871	26	34	32.84	0.0018	ctrl only
I3LJ87	Uncharacterized protein	RPS2	22515	247	257	37.03	0.001	ctrl only
A0A287ACL6	40S ribosomal protein S24	RPS24	34741	69	83	20.18	0.013	ctrl only
A0A287AZA7	Uncharacterized protein	RPS27A	8862	64	72	49.49	0.00039	both
Q0Z8U2	40S ribosomal protein S3	RPS3	12425	188	197	25.57	0.0075	ctrl only
A0A287B771	40S ribosomal protein S4	RPS4X	14712	117	127	34.4	0.0022	ctrl only
A0A287BCW5	40S ribosomal protein S6	RPS6	17641	82	93	29.49	0.0045	ctrl only
A0A287A993	Non-specific serine/threonine protein kinase	RPS6KA2	4720	44	52	34.91	0.0077	both
A0A287A9Y6	40S ribosomal protein S7	RPS7	7413	170	178	28.86	0.017	ctrl only
F2Z5F5	40S ribosomal protein S8	RPS8	27773	158	170	53.54	1.50E-05	ctrl only
A0A287B2M3	40S ribosomal protein SA	RPSA	10305	2	11	50.25	4.30E-05	ctrl only
P80310	Protein S100-A12	S100A12	41854	57	72	64.12	9.70E-07	both
F1SFV7	Protein S100	S100A4	8170	58	66	45.57	5.30E-05	ctrl only
C3S7K5	Protein S100	S100A8	24150	78	89	27.42	0.0034	both
C3S7K6	Calcium-binding protein A9	S100A9	19670	86	96	36.28	0.00065	both
F1SQR2	Protein S100	S100G	22520	63	74	30.85	0.0013	both
I3LIS0	Sphingosine-1-phosphate receptor 1	S1PR1	12547	284	292	28.21	0.018	ctrl only
F1S8F0	Uncharacterized protein	S1PR4	32351	88	103	16.94	0.049	ctrl only
A0A287AKL0	Serum amyloid A protein	SAA3	1897	60	68	29.86	0.0028	both
F1S9B8	Serum amyloid A protein	SAA4	15308	27	37	57.12	8.20E-05	both

Table 5: detailed information on the proteins identified in the input plasma proteome (continued).

prot_acc	prot_desc	gene_name	pep_query	pep_start	pep_end	pep_score	pep_expect	group
A0A286ZLW6	Uncharacterized protein	SAFB	5626	673	679	16.44	0.042	both
A0A287A7Z0	Uncharacterized protein	SAPCD2	3250	291	298	27.08	0.018	ctrl only
A0A287AR98	Uncharacterized protein	SBSN	30344	403	416	20.8	0.027	LPS only
A0A286ZNJ7	Uncharacterized protein	SEC63	9344	303	311	16.52	0.032	LPS only
A0A286ZRR3	Uncharacterized protein	SELENBP1	8271	394	401	20.45	0.024	ctrl only
I3LJP2	Uncharacterized protein	SELENOP	8434	132	139	27.77	0.0039	both
A0A288CG53	L-selectin	SELL	53265	82	98	27.28	0.0028	both
A0A287AX45	Uncharacterized protein	SEMA3D	46	82	87	24.77	0.041	both
A0A286ZJ16	Uncharacterized protein	SEPTIN7	53811	314	328	22.97	0.012	ctrl only
P50447	Alpha-1-antitrypsin	SERPINA1	1057	245	250	23.92	0.049	both
F1SCD1	Uncharacterized protein	SERPINA3-2	931	190	195	30.53	0.043	both
A0A287BHS2	Uncharacterized protein	SERPINA5	9255	47	54	25.65	0.008	both
F1SCF1	Uncharacterized protein	SERPINA6	25710	290	302	15.71	0.04	both
F1RXM6	Thyroxine-binding globulin	SERPINA7	1436	399	405	30.5	0.027	both
A0A287B7P2	Leukocyte elastase inhibitor	SERPINB1	27462	179	193	46.82	4.10E-05	both
F2Z5E2	Uncharacterized protein	SERPINC1	2348	141	147	45.12	0.0018	both
F1RKY2	Serpin family D member 1	SERPIND1	1997	428	434	33.91	0.0076	both
Q0PM28	Pigment epithelium-derived factor	SERPINF1	3742	239	246	27.29	0.013	both
A0A287AJI4	Uncharacterized protein	SERPINF2	4170	75	82	37.78	0.0049	both
F1SJW8	Uncharacterized protein	SERPING1	2631	479	485	21.38	0.039	both
A0A286ZRU9	Uncharacterized protein	SERPINH1	20387	320	332	22.69	0.033	ctrl only
F1RR69	Uncharacterized protein	SET	39910	124	137	22.69	0.013	ctrl only
A0A287A4F2	Uncharacterized protein	SFPQ	37380	475	488	22.86	0.0094	ctrl only
A0A287BPZ1	Pulmonary surfactant-associated protein D	SFTPD	27413	153	167	21.88	0.025	LPS only
A0A287A0P2	Small glutamine rich tetratricopeptide repeat containing beta	SGTB	909	145	151	34.45	0.022	ctrl only
A0A286ZWS0	SH3 domain-binding glutamic acid-rich-like protein	SH3BGRL3	37784	33	47	20.07	0.036	ctrl only
A0A286ZK02	Uncharacterized protein	SH3TC1	46815	319	334	18.68	0.032	ctrl only
F1RYS7	Uncharacterized protein	SHROOM3	42168	412	426	18.97	0.037	LPS only
A0A287B920	Sucrase-isomaltase intestinal	SI	767	596	601	22.49	0.041	ctrl only
A0A286ZKF2	Uncharacterized protein	SKIV2L	18330	672	682	19.45	0.015	ctrl only
F1SE25	Phosphate transporter	SLC20A2	9593	425	434	21.06	0.046	both
I3LPU7	Uncharacterized protein	SLC22A14	33885	1	12	27.38	0.035	both
F1RK74	Uncharacterized protein	SLC25A1	5217	9	19	21.71	0.043	ctrl only
A0A287BR27	Uncharacterized protein	SLC25A27	5959	153	160	17.58	0.035	ctrl only
A0A286ZIE8	Uncharacterized protein	SLC25A4	14864	11	23	29.05	0.005	ctrl only
F1RLI6	Uncharacterized protein	SLC25A46	10884	215	223	15.27	0.037	LPS only
F2Z565	Uncharacterized protein	SLC25A5	10977	64	72	26.51	0.012	ctrl only
Q6QRN9	ADP/ATP translocase 3	SLC25A6	10977	64	72	26.51	0.012	ctrl only
I3LCQ6	Uncharacterized protein	SLC39A2	1420	79	84	27.39	0.023	both
A0A2C9F351	Choline transporter-like protein 4	SLC44A4	2046	413	420	17.4	0.047	ctrl only
F1RQY6	Anion exchange protein	SLC4A1	1210	326	332	35.55	0.027	both
A0A287AMX1	Anion exchange protein	SLC4A2	897	368	373	40.13	0.0099	both
F1S024	Transporter	SLC6A3	1679	20	27	16.08	0.044	both
K9J4W3	Transporter	SLC6A6	28501	576	587	17.34	0.034	ctrl only
A0A287BFZ4	Uncharacterized protein	SLF2	33478	414	426	15.22	0.037	LPS only
A0A287BR93	Structural maintenance of chromosomes protein	SMC1B	2343	593	599	20.65	0.043	LPS only
A0A287AGI4	Uncharacterized protein	SMC2	16946	910	919	25.38	0.033	ctrl only
I3LCG7	Small integral membrane protein 26	SMIM26	5907	6	12	15.5	0.035	LPS only
A0A287BQT0	Uncharacterized protein	SMPDL3B	50940	283	298	34.78	0.00055	both
A7YX24	Gamma-synuclein	SNCG	5004	35	43	46.27	0.00022	both
A0A287A447	Uncharacterized protein	SNX30	1726	355	361	41.11	0.003	LPS only
P04178	Superoxide dismutase [Cu-Zn]	SOD1	4472	28	36	51.91	0.00039	ctrl only
I3LUD1	Superoxide dismutase [Cu-Zn]	SOD3	28817	101	112	17.32	0.024	both
A0A286ZZ32	Uncharacterized protein	SOGA3	702	59	66	16.5	0.028	LPS only
A0A1P0REP6	Spastin	SPAST	24844	266	279	19.96	0.028	ctrl only
A0A286ZT43	Uncharacterized protein	SPATA13	16228	1070	1078	30.81	0.008	LPS only
I3LER8	Uncharacterized protein	SPG11	216	2	6	37.38	0.0091	LPS only
P14287	Osteopontin	SPP1	20539	206	217	22.43	0.0086	both
Q711S8	Secreted phosphoprotein 24	SPP2	4494	121	127	59.55	4.80E-05	both
F1RNB8	Uncharacterized protein	SPTA1	6341	718	726	25.47	0.035	both
A0A287A113	Spectrin beta chain	SPTB	3199	681	687	40.1	0.0061	ctrl only
A0A286ZNC7	Spectrin beta chain	SPTBN1	16267	215	224	24.91	0.035	both
I3LKI1	Uncharacterized protein	SR	23141	53	65	52.99	0.00013	ctrl only
A0A286ZM20	Uncharacterized protein	SRRM1	7130	103	110	20.74	0.041	both
A0A286ZSZ6	Uncharacterized protein	SRRM2	6196	2723	2730	27.01	0.046	both
A0A286ZX74	Uncharacterized protein	SRSF5	8268	2	10	21.34	0.011	both
A0A287ASZ5	Uncharacterized protein	SRSF7	32446	45	58	31.15	0.0012	ctrl only
A0A287AT90	Uncharacterized protein	SSH1	13029	934	944	18.73	0.05	both
A0A287B8B1	Uncharacterized protein	ST13	21804	211	222	23.96	0.0057	both
A0A286ZSQ8	ST6 beta-galactoside alpha-2 6-sialyltransferase 1	ST6GAL1	67108	50	73	19.64	0.014	ctrl only
A0A286ZTH4	Uncharacterized protein	STIL	10515	1199	1207	16.33	0.045	ctrl only
I3LNG8	Stress induced phosphoprotein 1	STIP1	10177	534	543	36.84	0.00081	ctrl only
A5A8W9	Serine/threonine kinase 19	STK19	28863	8	19	21.67	0.018	LPS only
F1ST91	Uncharacterized protein	STK31	62352	337	355	18.18	0.028	both
A0A287AE47	Uncharacterized protein	STOM	4074	145	152	19.92	0.014	ctrl only
K9J6J2	Erythrocyte band 7 integral membrane protein isoform a	STOM_tv1	4074	145	152	19.92	0.014	ctrl only
A0A287AD21	Small ubiquitin-related modifier	SUMO3	15439	21	32	29.07	0.0023	ctrl only
F1S8K5	SPT16 homolog facilitates chromatin remodeling subunit	SUPT16H	19862	383	393	19.92	0.019	ctrl only
F1SNY4	Uncharacterized protein	TAB1	7091	218	227	23.41	0.046	ctrl only
A0A287BAJ9	Transcriptional adapter	TADA2A	5166	106	112	16.64	0.045	ctrl only
F1RJ93	Transgelin	TAGLN2	14714	128	139	71.77	9.70E-07	ctrl only
A0A287BQ72	Transaldolase	TALDO1	30608	72	86	57.76	3.80E-06	ctrl only
F1SP18	Uncharacterized protein	TARS	19030	541	552	21.35	0.0099	ctrl only
I3LCT3	Uncharacterized protein	TAS2R39	16881	1	10	19.15	0.016	ctrl only
F1RWJ4	TBK1 binding protein 1	TBKBP1	6741	95	103	24.27	0.031	ctrl only
A0A287AJY2	Uncharacterized protein	TCP1	14321	494	504	71.48	1.20E-06	ctrl only
A0A287AZ97	Uncharacterized protein	TDRD7	15637	258	268	16.43	0.029	ctrl only
P09571	Serotransferrin	TF	946	537	543	34.17	0.03	both
A0A287A3E7	Transferrin receptor protein 1	TFRC	41329	448	461	41.8	0.00014	both
F1RHA7	Transforming growth factor-beta-induced protein ig-h3	TGFBI	1941	179	185	28.79	0.02	both
F1SS26	Uncharacterized protein	THBS1	8680	75	83	31.82	0.039	both
A0A287AQ98	Uncharacterized protein	THBS2	5932	1035	1041	26.09	0.0047	both
A0A287AK31	Uncharacterized protein	THBS3	33734	811	823	69.28	1.60E-06	both
F1RF27	Uncharacterized protein	THBS4	33734	817	829	69.28	1.60E-06	both
F1SHM4	Uncharacterized protein	TIAM1	3013	2	8	39.06	0.0048	both
A8U4R4	Transketolase	tkt	4810	335	343	44.03	0.00041	ctrl only
A0A287AC34	Uncharacterized protein	TLN1	34364	2215	2227	19.13	0.029	LPS only
I3LPE4	Uncharacterized protein	TLR10	3889	188	194	19.95	0.013	LPS only
F1SN29	Uncharacterized protein	TMEFF2	3343	2	8	15.96	0.036	ctrl only
A0A287AKT1	Transmembrane protein 161A	TMEM161A	3067	150	156	16.8	0.027	LPS only
F1RLI7	Uncharacterized protein	TMEM232	61501	368	388	17.03	0.025	both
A0A286ZYQ9	Transmembrane protein 52B	TMEM52B	29	133	137	30.9	0.025	both
A0A287BJ41	Tropomodulin 1	TMOD1	35080	256	271	71.12	8.70E-07	ctrl only
I3LN91	Uncharacterized protein	TMTC2	73487	599	621	16.17	0.044	both
A0A286ZR70	Tenascin	TNC	27166	253	264	30.53	0.0043	LPS only
P02587	Troponin C skeletal muscle	TNNC2	1766	38	44	28.89	0.017	ctrl only
K7GRK7	Uncharacterized protein	TNXB	71669	4017	4039	37.93	0.00028	both
A0A288CFT0	Triosephosphate isomerase	TPI1	19889	244	256	61.98	4.40E-06	both
P42639	Tropomyosin alpha-1 chain	TPM1	15795	92	101	72.59	3.30E-06	both

Table 5: detailed information on the proteins identified in the input plasma proteome (continued).

prot_acc	prot_desc	gene_name	pep_query	pep_start	pep_end	pep_score	pep_expect	group
A0A287AD38	Uncharacterized protein	TPM2	12961	169	178	34.68	0.00056	ctrl only
A1XQV4	Tropomyosin alpha-3 chain	TPM3	12389	169	178	39.1	0.0045	ctrl only
P67937	Tropomyosin alpha-4 chain	TPM4	7971	2	11	29.67	0.0035	both
A0A287B4E6	Translationally-controlled tumor protein	TPT1	35721	6	19	30.35	0.0014	ctrl only
A0A286ZLB1	Uncharacterized protein	TRAP1	28098	387	400	90.08	1.10E-08	ctrl only
A0A286ZR41	Uncharacterized protein	TRAPPC10	10066	724	731	15.16	0.045	ctrl only
A0A287BNT0	Uncharacterized protein	TRPC1	50611	51	65	16.8	0.044	ctrl only
A0A287A4K8	Transient receptor potential cation channel subfamily M member 4	TRPM4	52438	195	213	16.54	0.028	ctrl only
F1S497	Uncharacterized protein	TTC9	7831	203	210	21.01	0.031	both
F1SAY2	Uncharacterized protein	TTF2	25593	991	1003	18.5	0.039	LPS only
P50390	Transthyretin	TTR	388	36	41	36.6	0.016	both
P02550	Tubulin alpha-1A chain	TUBA1A	23543	85	96	36.11	0.00072	ctrl only
A0A286ZNY1	Tubulin alpha chain	TUBA4A	23543	85	96	36.11	0.00072	ctrl only
A0A287B5H5	Tubulin alpha chain	TUBA8	23543	79	90	36.11	0.00072	ctrl only
F2Z5B2	Tubulin beta chain	TUBB	11323	242	251	42.97	0.0002	ctrl only
A5GFX6	Tubulin beta chain	TUBB1	11323	242	251	42.97	0.0002	ctrl only
F1S6M7	Tubulin beta chain	TUBB3	11323	242	251	42.97	0.0002	ctrl only
F2Z5K5	Tubulin beta chain	TUBB4A	11323	242	251	42.97	0.0002	ctrl only
A0A287A217	Tubulin beta chain	TUBB4B	11323	262	271	42.97	0.0002	ctrl only
A0A287B749	Tubulin beta chain	TUBB6	11323	242	251	42.97	0.0002	ctrl only
A0A287B1K1	Gamma-tubulin complex component	TUBGCP5	8438	2	10	18.79	0.024	LPS only
A0A287AXA3	Uncharacterized protein	TULP4	12998	558	567	19.5	0.046	both
A0A287BFL6	Uncharacterized protein	TXLNG	8162	409	417	27.85	0.0066	ctrl only
P82460	Thioredoxin	TXN	16997	95	105	23.63	0.024	both
A0A286ZJ07	Uncharacterized protein	TXNRD2	14054	223	233	22.76	0.019	ctrl only
K7GRY0	Ubiquitin like modifier activating enzyme 1	UBA1	17870	1011	1021	36.16	0.014	both
B8Y648	Ubiquitin-conjugating enzyme E2L 3	UBE2L3	38229	53	67	28.54	0.0021	ctrl only
A0A287B778	Uncharacterized protein	UBE2O	41823	930	946	17.59	0.045	ctrl only
A0A287BSL7	Uncharacterized protein	UBE2V1	11224	54	63	28.23	0.0087	ctrl only
A0A287AHL7	Uncharacterized protein	UBTD1	22415	163	175	19.05	0.033	ctrl only
F1S0D8	Uncharacterized protein	UBXN4	34274	2	16	15.42	0.048	ctrl only
A0A287BRT0	Ubiquitin carboxyl-terminal hydrolase	UCHL3	27998	122	134	57.29	1.40E-05	ctrl only
A0A287B0N8	Uncharacterized protein	UNC5D	2304	1	6	25.26	0.049	ctrl only
F1SSS4	Uncharacterized protein	UNC80	39536	967	981	16.68	0.038	ctrl only
A0A287AVG2	Uncharacterized protein	URGCP	480	393	398	25.11	0.004	both
A0A287B6R5	Uncharacterized protein	USH2A	3270	3103	3110	24.83	0.012	both
I3L945	Uncharacterized protein	USP14	21865	31	43	30.64	0.0013	ctrl only
I3L8M9	Uncharacterized protein	USP25	12671	823	831	16.27	0.048	both
A0A287A103	Uncharacterized protein	USP4	6266	172	179	31.04	0.048	ctrl only
F1RUW2	Ubiquitinyl hydrolase 1	USP49	37114	97	112	17.99	0.031	both
F1SF51	Uncharacterized protein	UTP25	291	75	80	32.6	0.038	ctrl only
A0A287A1Y2	Uncharacterized protein	VANGL1	3453	379	386	28.94	0.027	both
A0A287BPW4	Uncharacterized protein	VARS	10113	174	182	22.03	0.018	both
I3LS87	Vasorin	VASN	14755	487	496	39.32	0.0012	both
F1S567	Uncharacterized protein	VCAM1	15680	300	310	51.69	4.40E-05	both
A0A287BSL4	Vinculin	VCL	10907	656	666	43.34	0.00027	both
P03974	Transitional endoplasmic reticulum ATPase	VCP	4869	148	155	33.71	0.0048	both
A0A2C9F3B2	Voltage-dependent anion-selective channel protein 1	VDAC1	19652	1	12	23.48	0.041	ctrl only
Q9MZ15	Voltage-dependent anion-selective channel protein 2	VDAC2	56979	186	208	15.59	0.034	ctrl only
A0A2C9F3D9	Vimentin	VIM	3005	114	120	36	0.0012	ctrl only
F1S3Q8	Uncharacterized protein	VNN3	5354	49	56	20.88	0.011	both
A0A286ZW46	Uncharacterized protein	VPS36	37199	204	216	22.98	0.018	LPS only
I3L638	Vitronectin	VTN	646	247	251	35.1	0.028	both
Q28833	von Willebrand factor (Fragment)	VWF	6800	651	659	16.09	0.031	both
A0A286ZYC8	Uncharacterized protein	WAP-3	22222	52	63	28.92	0.0087	both
A0A287A1J0	Protein Wnt	WNT5A	26796	216	227	17.64	0.046	LPS only
A0A287A1D2	Uncharacterized protein	XPO1	1999	385	391	22.8	0.044	ctrl only
F1SDR7	Uncharacterized protein	YWHAB	49263	141	159	109.78	5.10E-11	ctrl only
A0A287A2R9	Uncharacterized protein	YWHAE	15539	107	118	52.24	2.40E-05	both
A0A287AXR5	Uncharacterized protein	YWHAZ	17362	128	139	46.02	0.00015	ctrl only
A0A286ZTI8	Uncharacterized protein	ZBTB20	1539	342	347	39.95	0.0057	LPS only
F1RUB7	Uncharacterized protein	ZBTB33	22182	521	529	27.35	0.031	LPS only
F1S5G5	Uncharacterized protein	ZBTB49	31297	488	500	24.08	0.024	both
M3UZ00	Zinc finger CCCH-type containing 18	ZC3H18	167	895	900	38.64	0.01	both
F1S7I8	Uncharacterized protein	ZCCHC3	66275	378	402	15.99	0.048	ctrl only
A4U9C9	Zinc finger protein 216	ZFAND5	60040	87	111	17.4	0.023	ctrl only
A0A287BAB1	Zinc finger RNA binding protein	ZFR	18737	756	766	19.73	0.036	LPS only
F1RR15	Zinc fingers and homeoboxes 1	ZHX1	7560	181	188	19.96	0.021	LPS only
I3LP64	Uncharacterized protein	ZKSCAN2	15	929	934	32.5	0.049	ctrl only
F1RFI5	Zinc finger protein 48	ZNF48	1149	519	524	26.1	0.019	ctrl only
F1S2F2	Uncharacterized protein	ZNF503	30277	1	14	21.28	0.012	LPS only
F1SC29	Uncharacterized protein	ZNF518A	133	444	448	24.54	0.047	ctrl only
A0A287BJQ8	Uncharacterized protein	ZNF691	201	62	67	36.69	0.0093	ctrl only
A0A287A5E4	Uncharacterized protein	ZNF783	19196	1	12	21.69	0.0092	ctrl only

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